Breast Cancer Progression Signatures

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FIELD OF THE INVENTION

The invention relates to the identification and use of gene expression profiles, or patterns, involved in breast cancer progression. The gene expression profiles, whether embodied in nucleic acid expression, protein expression, or other expression formats, are used in the study and/or diagnosis of cells and tissue during breast cancer progression as well as for the study and/or determination of prognosis of a patient. When used for diagnosis or prognosis, the profiles are used to predict the status and/or phenotype of cells and tissues relative to breast cancer and the treatment thereof.

BACKGROUND OF THE INVENTION

Breast cancer is by far the most common cancer among women. Each year, more than 180,000 and 1 million women in the U.S. and worldwide, respectively, are diagnosed with breast cancer. Breast cancer is the leading cause of death for women between ages 50-55, and is the most common non-preventable malignancy in women in the Western Hemisphere. An estimated 2,167,000 women in the United States are currently living with the disease (National Cancer Institute, Surveillance Epidemiology and End Results (NCI SEER) program, *Cancer Statistics*

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Review (CSR), www-seer.ims.nci.nih.gov/Publications/CSR1973 (1998)). Based on cancer rates from 1995 through 1997, a report from the National Cancer Institute (NCI) estimates that about 1 in 8 women in the United States (approximately 12.8 percent) will develop breast cancer during her lifetime (NCI's Surveillance, Epidemiology, and End Results Program (SEER) publication *SEER Cancer Statistics Review 1973-1997)*. Breast cancer is the second most common form of cancer, after skin cancer, among women in the United States. An estimated 250,100 new cases of breast cancer are expected to be diagnosed in the United States in 2001. Of these, 192,200 new cases of more advanced (invasive) breast cancer are expected to occur among women (an increase of 5% over last year), 46,400 new cases of early stage (*in situ*) breast cancer are expected to occur among women (up 9% from last year), and about 1,500 new cases of breast cancer are expected to be diagnosed in men (Cancer Facts & Figures 2001 American Cancer Society). An estimated 40,600 deaths (40,300 women, 400 men) from breast cancer are expected in 2001. Breast cancer ranks second only to lung cancer among causes of cancer deaths in women. Nearly 86% of women who are diagnosed with breast cancer are likely to still be alive five years later, though 24% of them will die of breast cancer after 10 years, and nearly half (47%) will die of breast cancer after 20 years.

Every woman is at risk for breast cancer. Over 70 percent of breast cancers occur in women who have no identifiable risk factors other than age (U.S. General Accounting Office. Breast Cancer, 1971-1991: Prevention, Treatment and Research. GAO/PEMD-92-12; 1991). Only 5 to 10% of breast cancers are linked to a family history of breast cancer (Henderson IC, Breast Cancer. In: Murphy GP, Lawrence WL, Lenhard RE (eds). *Clinical Oncology*. Atlanta, GA: American Cancer Society; 1995:198-219).

Each breast has 15 to 20 sections called lobes. Within each lobe are many smaller lobules. Lobules end in dozens of tiny bulbs that can produce milk. The lobes, lobules, and bulbs are all linked by thin tubes called ducts. These ducts lead to the nipple in the center of a dark area of skin called the areola. Fat surrounds the lobules and ducts. There are no muscles in the breast, but muscles lie under each breast and cover the ribs. Each breast also contains blood

vessels and lymph vessels. The lymph vessels carry colorless fluid called lymph, and lead to the lymph nodes. Clusters of lymph nodes are found near the breast in the axilla (under the arm), above the collarbone, and in the chest.

Breast tumors can be either benign or malignant. Benign tumors are not cancerous, they do not spread to other parts of the body, and are not a threat to life. They can usually be removed, and in most cases, do not come back. Malignant tumors are cancerous, and can invade and damage nearby tissues and organs. Malignant tumor cells may metastisize, entering the bloodstream or lymphatic system. When breast cancer cells metastisize outside the breast, they are often found in the lymph nodes under the arm (axillary lymph nodes). If the cancer has reached these nodes, it means that cancer cells may have spread to other lymph nodes or other organs, such as bones, liver, or lungs.

Major and intensive research has been focussed on early detection, treatment and prevention. This has included an emphasis on determining the presence of precancerous or cancerous ductal epithelial cells. These cells are analyzed, for example, for cell morphology, for protein markers, for nucleic acid markers, for chromosomal abnormalities, for biochemical markers, and for other characteristic changes that would signal the presence of cancerous or precancerous cells. This has led to various molecular alterations that have been reported in breast cancer, few of which have been well characterized in human clinical breast specimens. Molecular alterations include presence/absence of estrogen and progesterone steroid receptors, HER-2 expression/amplification (Mark HF, et al. HER-2/neu gene amplification in stages I-IV breast cancer detected by fluorescent in situ hybridization. Genet Med; 1(3):98-103 1999), Ki-67 (an antigen that is present in all stages of the cell cycle except G0 and used as a marker for tumor cell proliferation, and prognostic markers (including oncogenes, tumor suppressor genes, and angiogenesis markers) like p53, p27, Cathepsin D, pS2, multi-drug resistance (MDR) gene, and CD31.

Examination of cells by a trained pathologist has also been used to establish whether ductal epithelial cells are normal (i.e. not precancerous or cancerous or having another

noncancerous abnormality), precancerous (i.e. comprising hyperplasia, atypical ductal hyperplasia (ADH)) or cancerous (comprising ductal carcinoma *in situ*, or DCIS, which includes low grade ductal carcinoma *in situ*, or LG-DCIS, and high grade ductal carcinoma in situ, or HG-DCIS) or invasive (ductal) carcinoma (IDC). Pathologists may also identify the occurrence of lobular carcinoma in situ (LCIS) or invasive lobular carcinoma (ILC). Breast cancer progression may be viewed as the occurrence of abnormal cells, such as those of ADH, DCIS, IDC, LCIS, and/or ILC, among normal cells.

It remains unclear whether normal cells become hyperplastic (such as ADH) and then progressing on to become malignant (DCIS, IDC, LCIS, and/or ILC) or whether normal cells are able to directly become malignant without transitioning through a hyperplastic stage. It has been observed, however, that the presence of ADH indicates a higher likelihood of developing a malignancy. This has resulting in treatment of patients with ADH to begin treatment with an antineoplastic/antitumor agent such as tamoxifen. This is in contrast to the treatment of patients with malignant breast cancer which usually includes surgical removal.

The rational development of preventive, diagnostic and therapeutic strategies for women at risk for breast cancer would be aided by a molecular map of the tumorigenesis process. Relatively little is known of the molecular events that mediate the transition of normal breast cells to the various stages of breast cancer progression. In particular, there is a significant paucity of information regarding the genetic changes that are associated with the earliest stages of human breast cancer, which include the transition of normal breast cells to atypical hyperplastic and/or pre-invasive malignant cells (carcinoma *in situ*).

Molecular means of identifying the differences between normal, non-cancerous cells and cancerous cells (in general) have also been the focus of intense study. The use of cDNA libraries to analyze differences in gene expression patterns in normal versus tumorigenic cells has been described (USP 4,981,783). DeRisi et al. (1996) describe the analysis of gene expression patterns between two cell lines: UACC-903, which is a tumorigenic human melanoma cell line, and UACC-903(+6), which is a chromosome 6 suppressed non-tumorigenic form of UACC-903.

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Labeled cDNA probes made from mRNA from these cell lines were applied to DNA microarrays containing 870 different cDNAs and controls. Genes that were preferentially expressed in one of the two cell lines were identified.

Golub et al. (1999) describe the use of gene expression monitoring as means to cancer class discovery and class prediction between acute myeloid leukemia (AML) and acute lymphoblastic leukemia (ALL). Their approach to class predictors used a neighborhood analysis followed by cross-validation of the validity of the predictors by withholding one sample and building a predictor based only on the remaining samples. This predictor is then used to predict the class of the withheld sample. They also used cluster analysis to identify new classes (or subtypes) within the AML and ALL.

Gene expression patterns in human breast cancers have been described by Perou et al. (1999), who studied gene expression between cultured human mammary epithelia cells (HMEC) and breast tissue samples by use of microarrays comprising about 5000 genes. They used a clustering algorithm to identify patterns of expression in HMEC and tissue samples. Perou et al. (2000) describe the use of clustered gene expression profiles to classify subtypes of human breast tumors. Hedenfalk et al. describe gene expression profiles in BRCA1 mutation positive, BRCA2 mutation positive, and sporadic tumors. Sgroi et al. also analyzed gene expression of normal and breast cancer cells from a single patient. Using gene expression patterns to distinguish breast tumor subclasses and predict clinical implications is described by Sorlie et al. and West et al.

All of the above described approaches, however, utilize heterogeneous populations of cells found in culture or in a biopsy to obtain information on gene expression patterns. The use of such populations may result in the inclusion or exclusion of multiple genes from the patterns. For this and the lack of statistical robustness reasons, the gene expression patterns observed by the above described approaches provide little confidence that the differences in gene expression may be meaningfully associated with the stages of breast cancer.

SUMMARY OF THE INVENTION

The present invention relates to the identification and use of gene expression patterns (or profiles or "signatures") which are correlated with (and thus able to discriminate between) cells in various stages of breast cancer. Broadly defined, these stages are non-malignant versus malignant, but may also be viewed as normal versus atypical (optionally including reactive and pre-neoplastic) versus cancerous. Another definition of the stages is normal versus precancerous (e.g. atypical ductal hyperplasia (ADH) or atypical lobular hyperplasia (ALH)) versus cancerous (e.g. carcinoma *in situ* such as DCIS and/or LCIS) versus invasive (e.g. carcinomas such as IDC and/or ILC). DCIS may be further viewed as low grade versus high grade or grade I through grade III.

The gene expression patterns comprise one or more than one gene capable of discriminating between various stages of breast cancer with significant accuracy. The gene(s) are identified as correlated with various stages of breast cancer such that the levels of their expression are relevant to a determination of the stage of breast cancer of a cell. Thus in one aspect, the invention provides a method to determine the stage of breast cancer of a subject afflicted with, or suspected of having, breast cancer by assaying a cell containing sample from said subject for expression of one or more than one gene disclosed herein as correlated with one or more stages of breast cancer.

Gene expression patterns of the invention are identified by analysis of gene expression in multiple samples of each stage to be studied. The overall gene expression profile of each sample is obtained by analyzing the expressed or unexpressed state of genes in each stage relative to each other (one gene to another across all genes). This overall profile is then analyzed to identify genes that are positively, or negatively, correlated, with a stage of breast cancer relative to other genes. An expression profile of a subset of human genes may then be identified by the methods of the present invention as correlated with breast cancer. The use of multiple samples increases the confidence which which a gene may be believed to be correlated with a particular stage.

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Without sufficient confidence, it remains unpredictable whether a particular gene is actually correlated with a stage of breast cancer and also unpredictable whether a particular gene may be successfully used to identify the stage of an unknown breast cancer cell sample.

A profile of genes that are highly correlated with one stage relative to another may be used to assay an sample from a subject afflicted with, or suspected of having, breast cancer to identify the stage of breast cancer to which the sample belongs. Such an assay may be used as part of a method to determine the therapeutic treatment for said subject based upon the stage(s) of breast cancer identified.

The correlated genes may be used singly with significant accuracy or in combination to increase the ability to accurately discriminate between various stages of breast cancer. The present invention thus provides means for correlating a molecular expression phenotype with a physiological (cellular) stage or state. This correlation provides a way to molecularly diagnose and/or monitor a cell's status in comparison to different cancerous versus non-cancerous phenotypes as disclosed herein. Additional uses of the correlated gene(s) are in the classification of cells and tissues; determination of diagnosis and/or prognosis; and determination and/or alteration of therapy.

The ability to discriminate is conferred by the identification of expression of the individual genes as relevant and not by the form of the assay used to determine the actual level of expression. An assay may utilize any identifying feature of an identified individual gene as disclosed herein as long as the assay reflects, quantitatively or qualitatively, expression of the gene. Identifying features include, but are not limited to, unique nucleic acid sequences used to encode (DNA), or express (RNA), said gene or epitopes specific to, or activities of, a protein encoded by said gene. All that is required is the identity of the gene(s) necessary to discriminate between stages of breast cancer and an appropriate cell containing sample for use in an expression assay.

In one aspect, the invention provides for the identification of the gene expression patterns by analyzing global, or near global, gene expression from single cells or homogenous cell

populations which have been dissected away from, or otherwise isolated or purified from, contaminating cells beyond that possible by a simple biopsy. Because the expression of numerous genes fluctuate between cells from different patients as well as between cells from the same patient sample, multiple individual gene expression patterns are used as reference data to generate models which in turn permit the identification of individual gene(s) that are most highly correlated with particular breast cancer stages and/or have the best the ability to discriminate cells of one stage from another.

In another aspect, the invention provides physical and methodological means for detecting the expression of gene(s) identified by the models generated by individual expression patterns. These means may be directed to assaying one or more aspect of the DNA template(s) underlying the expression of the gene(s), of the RNA used as an intermediate to express the gene(s), or of the proteinaceous product expressed by the gene(s).

In a further aspect, the gene(s) identified by a model as capable of discriminating between breast cancer stages may be used to identify the cellular state of an unknown sample of cell(s) from the breast. Preferably, the sample is isolated via non-invasive means. The expression of said gene(s) in said unknown sample may be determined and compared to the expression of said gene(s) in reference data of gene expression patterns from the various stages of breast cancer. Optionally, the comparison to reference samples may be by comparison to the model(s) constructed based on the reference samples.

One advantage provided by the present invention is that contaminating, non-breast cells (such as infiltrating lymphocytes or other immune system cells) are not present to possibly affect the genes identified or the subsequent analysis of gene expression to identify the status of suspected breast cancer cells. Such contamination is present where a biopsy is used to generate gene expression profiles.

While the present invention has been described mainly in the context of human breast cancer, it may be practiced in the context of breast cancer of any animal known to be potentially afflicted by breast cancer. Preferred animals for the application of the present invention are

mammals, particularly those important to agricultural applications (such as, but not limited to, cattle, sheep, horses, and other "farm animals") and for human companionship (such as, but not limited to, dogs and cats).

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a schematic representing a data matrix of a pair-wise comparison between Grade I and Grade III DCIS among 16 samples (across the top) and a large number of genes identified by "CloneID") along the left hand side.

Figure 2 is a table showing the actual weight data corresponding to Example II, where the data from ten genes (by CloneID number vertically) are compared to DCIS and ADH samples (across the top). Some data in the table has been vertically presented to permit the table to be displayed on a single sheet. The use of "-" with data in the table reflects genes that are more highly expressed in ADH relative to DCIS. The absence of "-" reflects genes that are more highly expressed in DCIS relative to ADH.

Figure 3 is a table showing the actual weight data corresponding to Example VII, where the data from over 300 genes (by CloneID number vertically) are compared to DCIS and ADH samples (across the top). Some data in the table has been vertically presented solely for display purposes. The use of "-" with data in the table reflects genes that are more highly expressed in ADH relative to DCIS. The absence of "-" reflects genes that are more highly expressed in DCIS relative to ADH.

Figure 4 is a table showing the actual weight data corresponding to Example VIII, where the data from over 300 genes (by CloneID number vertically) are compared to samples (across the top) from two grades of DCIS. The use of "-" with data in the table reflects genes that are more

highly expressed in grade I relative to grade III. The absence of "-" reflects genes that are more highly expressed in grade III relative to grade I.

DETAILED DESCRIPTION OF THE SPECIFIC EMBODIMENTS

Definitions of terms as used herein:

A gene expression "pattern" or "profile" or "signature" refers to the relative expression of a gene between two or more stages of breast cancer which is correlated with being able to distinguish between said stages.

A "gene" is a polynucleotide that encodes a discrete product, whether RNA or proteinaceous in nature. It is appreciated that more than one polynucleotide may be capable of encoding a discrete product. The term includes alleles and polymorphisms of a gene that encodes the same product, or a functionally associated (including gain, loss, or modulation of function) analog thereof, based upon chromosomal location and ability to recombine during normal mitosis.

A "stage" or "stages" (or equivalents thereof) of breast cancer refer to a physiologic state of a breast cell as defined by known cytological or histological (including immunohistology, histochemistry, and immunohistochemistry) procedures and are readily known to skilled in the art. Non-limiting examples include normal versus abnormal, non-cancerous versus cancerous, the different stages described herein (e.g. hyperplastic, carcinoma, and invasive), and grades within different stages (e.g. grades I, II, or III or the equivalents thereof within cancerous stages).

The terms "correlate" or "correlation" or equivalents thereof refer to an association between expression of one or more genes and a physiologic state of a breast cell to the exclusion of one or more other stages and/or identified by use of the methods as described herein. A gene may be expressed at higher or lower levels and still be correlated with one or more breast cancer stages.

A "polynucleotide" is a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, this term includes double- and single-stranded DNA and RNA. It also includes known types of modifications including labels known in the art, methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, and internucleotide modifications such as uncharged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), as well as unmodified forms of the polynucleotide.

The term "amplify" is used in the broad sense to mean creating an amplification product can be made enzymatically with DNA or RNA polymerases. "Amplification," as used herein, generally refers to the process of producing multiple copies of a desired sequence, particularly those of a sample. "Multiple copies" mean at least 2 copies. A "copy" does not necessarily mean perfect sequence complementarity or identity to the template sequence.

By corresponding is meant that a nucleic acid molecule shares a substantial amount of sequence identity with another nucleic acid molecule. Substantial amount means at least 95%, usually at least 98% and more usually at least 99%, and sequence identity is determined using the BLAST algorithm, as described in Altschul et al. (1990), J. Mol. Biol. 215:403-410 (using the published default setting, i.e. parameters w=4, t=17). Methods for amplifying mRNA are generally known in the art, and include reverse transcription PCR (RT-PCR) and those described in U.S. Patent Application (number to be assigned) entitled "Nucleic Acid Amplification" filed on October 25, 2001 as attorney docket number 485772002900 as well as U.S. Provisional Patent Applications 60/298,847 (filed June 15, 2001) and 60/257,801 (filed December 22, 2000), all of which are hereby incorporated by reference in their entireties as if fully set forth. Alternatively, RNA may be directly labeled as the corresponding cDNA by methods known in the art.

A "microarray" is a linear or two-dimensional array of preferably discrete regions, each having a defined area, formed on the surface of a solid support such as, but not limited to, glass, plastic, or synthetic membrane. The density of the discrete regions on a microarray is

determined by the total numbers of immobilized polynucleotides to be detected on the surface of a single solid phase support, preferably at least about 50/cm^2, more preferably at least about 100/cm^2, even more preferably at least about 500/cm^2, but preferably below about 1,000/cm^2. Preferably, the arrays contain less than about 500, about 1000, about 1500, about 2000, about 2500, or about 3000 immobilized polynucleotides in total. As used herein, a DNA microarray is an array of oligonucleotides or polynucleotides placed on a chip or other surfaces used to hybridize to amplified or cloned polynucleotides from a sample. Since the position of each particular group of primers in the array is known, the identities of a sample polynucleotides can be determined based on their binding to a particular position in the microarray.

Because the invention relies upon the identification of genes that are over- or under-expressed, one embodiment of the invention involves determining expression by hybridization of mRNA, or an amplified or cloned version thereof, of a sample cell to a polynucleotide that is unique to a particular gene sequence. Preferred polynucleotides of this type contain at least about 20, at least about 22, at least about 24, at least about 26, at least about 28, at least about 30, or at least about 32 consecutive basepairs of a gene sequence that is not found in other gene sequences. The term "about" as used in the previous sentence refers to an increase or decrease of 1 from the stated numerical value. Even more preferred are polynucleotides of at least about 50, at least about 100, and at least about 150 basepairs of a gene sequence that is not found in other gene sequences. The term "about" as used in the preceding sentence refers to an increase or decrease of 10% from the stated numerical value.

Alternatively, and in another embodiment of the invention, gene expression may be determined by analysis of expressed protein in a cell sample of interest by use of one or more antibodies specific for one or more epitopes of individual gene products (proteins) in said cell sample. Such antibodies are preferably labeled to permit their easy detection after binding to the gene product.

The term "label" refers to a composition capable of producing a detectable signal indicative of the presence of the labeled molecule. Suitable labels include radioisotopes,

nucleotide chromophores, enzymes, substrates, fluorescent molecules, chemiluminescent moieties, magnetic particles, bioluminescent moieties, and the like. As such, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means.

The term "support" refers to conventional supports such as beads, particles, dipsticks, fibers, filters, membranes and silane or silicate supports such as glass slides.

As used herein, a "breast tissue sample" or "breast cell sample" refers to a sample of breast tissue or fluid isolated from an individual suspected of being afflicted with, or at risk of developing, breast cancer. Such samples are primary isolates (in contrast to cultured cells) and may be collected by any non-invasive means, including, but not limited to, ductal lavage, fine needle aspiration, needle biopsy, the devices and methods described in U.S. Patent 6,328,709, or any other suitable means recognized in the art. Alternatively, the "sample" may be collected by an invasive method, including, but not limited to, surgical biopsy.

"Expression" and "gene expression" include transcription and/or translation of nucleic acid material.

As used herein, the term "comprising" and its cognates are used in their inclusive sense; that is, equivalent to the term "including" and its corresponding cognates.

Conditions that "allow" an event to occur or conditions that are "suitable" for an event to occur, such as hybridization, strand extension, and the like, or "suitable" conditions are conditions that do not prevent such events from occurring. Thus, these conditions permit, enhance, facilitate, and/or are conducive to the event. Such conditions, known in the art and described herein, depend upon, for example, the nature of the nucleotide sequence, temperature, and buffer conditions. These conditions also depend on what event is desired, such as hybridization, cleavage, strand extension or transcription.

Sequence "mutation," as used herein, refers to any sequence alteration in the sequence of a gene disclosed herein interest in comparison to a reference sequence. A sequence mutation includes single nucleotide changes, or alterations of more than one nucleotide in a sequence, due

to mechanisms such as substitution, deletion or insertion. Single nucleotide polymorphism (SNP) is also a sequence mutation as used herein. Because the present invention is based on the relative level of gene expression, mutations in non-coding regions of genes as disclosed herein may also be assayed in the practice of the invention.

"Detection" includes any means of detecting, including direct and indirect detection of gene expression and changes therein. For example, "detectably less" products may be observed directly or indirectly, and the term indicates any reduction (including the absence of detectable signal). Similarly, "detectably more" product means any increase, whether observed directly or indirectly.

Unless defined otherwise all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

Specific Embodiments

The present invention relates to the identification and use of gene expression patterns (or profiles or "signatures") which discriminate between (or are correlated with) cells in various stages of breast cancer. Such patterns may be determined by the methods of the invention by use of a number of reference cell or tissue samples, such as those reviewed by a pathologist of ordinary skill in the pathology of breast cancer, which reflect various stages of breast cancer. Because the overall gene expression profile differs from person to person, cancer to cancer, and cancer cell to cancer cell, correlations between certain cell states and genes expressed or underexpressed may be made as disclosed herein to identify genes that are capable of discriminating between different breast cancer states.

The present invention may be practiced with any number of genes believed, or likely to be, differentially expressed in breast cancer cells. In Example I below, approximately 12,000 genes were used to identify hundreds of genes capable of discriminating between various stages of breast cancer as shown in Examples 2-9. The identification may be made by using expression

profiles of various homogenous normal and breast cancer cell populations, which were isolated by microdissection, such as, but not limited to, laser capture microdissection (LCM) of 100-1000 cells. Each gene of the expression profile may be assigned weights based on its ability to discriminate between two or more stages of breast cancer (see Example I). The magnitude of each assigned weight indicates the extent of difference in expression between the two groups and is an approximation of the ability of expression of the gene to discriminate between the two groups (and thus stages). The magnitude of each assigned weight also approximates the extent of correlation between expression of individual gene(s) and particular breast cancer stages.

It should be noted that merely high levels of expression in cells from a particular stage or stages does not necessarily mean that a gene will be identified as having a high absolute weight value.

Genes with top ranking weights (in absolute terms) may be used to generate models of gene expressions that would maximally discriminate between the two groups. Alternatively, genes with top ranking weights (in absolute terms) may be used in combination with genes with lower weights without signficant loss of ability to discriminate between groups. Such models may be generated by any appropriate means recognized in the art, including, but not limited to, cluster analysis, supported vector machines, neural networks or other algorithm known in the art. The models are capable of predicting the classification of a unknown sample based upon the expression of the genes used for discrimination in the models. "Leave one out" cross-validation may be used to test the performance of various models and to help identify weights (genes) that are uninformative or detrimental to the predictive ability of the models. Cross-validation may also be used to identify genes that enhance the predictive ability of the models.

The gene(s) identified as correlated with particular breast cancer stages by the above models provide the ability to focus gene expression analysis to only those genes that contribute to the ability to identify a cell as being in a particular stage of breast cancer relative to another stage or stages. The expression of other genes in a breast cancer cell would be relatively unable to provide information concerning, and thus assist in the discrimination of, different stages of

breast cancer. For example, the alpha subunit of human topoisomerase II (identified by CloneID 825470) has been found to be useful in discriminations between normal and atypical cells (ADH and DCIS and IDC and LCIS), between normal and ADH cells compared to DCIS and IDC cells, between normal and DCIS cells, between ADH and DCIS cells, between grade I and grade III DCIS cells, and between grade I and grade III IDC cells but not between normal and ADH cells (see Examples II to IX below). Thus expression of this topoisomerase II subunit would be utilized in models to discriminate between the above listed stages but not for discerning normal from ADH cells. This type of analysis is readily incorporated into algorithms used to generate models with reference gene expression data.

As will be appreciated by those skilled in the art, the models are highly useful with even a small set of reference gene expression data and can become increasingly accurate with the inclusion of more reference data although the incremental increase in accuracy will likely diminish with each additional datum. The preparation of additional reference gene expression data using genes identified and disclosed herein for discriminating between different stages of breast cancer is routine and may be readily performed by the skilled artisan to permit the generation of models as described above to predict the status of an unknown sample based upon the expression levels of those genes.

To determine the expression levels of genes in the practice of the present invention, any method known in the art may be utilized. In one preferred embodiment of the invention, expression based on detection of RNA which hybridizes to the genes identified and disclosed herein is used. This is readily performed by any RNA detection or amplification+detection method known or recognized as equivalent in the art such as, but not limited to, reverse transcription-PCR, the methods disclosed in U.S. Patent Application (number to be assigned) entitled "Nucleic Acid Amplification" filed on October 25, 2001 as attorney docket number 485772002900 as well as U.S. Provisional Patent Applications 60/298,847 (filed June 15, 2001) and 60/257,801 (filed December 22, 2000), and methods to detect the presence, or absence, of RNA stabilizing or destabilizing sequences.

Alternatively, expression based on detection of DNA status may be used. Detection of the DNA of an indentified gene as methylated or deleted may be used for genes that have decreased expression in correlation with a particular breast cancer stage. This may be readily performed by PCR based methods known in the art. Conversely, detection of the DNA of an indentified gene as amplified may be used for genes that have increased expression in correlation with a particular breast cancer stage. This may be readily performed by PCR based, fluorescent in situ hybridization (FISH) and chromosome in situ hybridization (CISH) methods known in the art.

Expression based on detection of a presence, increase, or decrease in protein levels or activity may also be used. Detection may be performed by any immunohistochemistry (IHC) based, blood based (especially for secreted proteins), antibody (including autoantibodies against the protein) based, ex foliate cell (from the cancer) based, mass spectroscopy based, and image (including used of labeled ligand) based method known in the art and recognized as appropriate for the detection of the protein. Antibody and image based methods are additionally useful for the localization of tumors after determination of cancer by use of cells obtained by a non-invasive procedure (such as ductal lavage or fine needle aspiration), where the source of the cancerous cells is not known. A labeled antibody or ligand may be used to localize the carcinoma(s) within a patient.

A preferred embodiment using a nucleic acid based assay to determine expression is by immobilization of one or more of the genes identified herein on a solid support, including, but not limited to, a solid substrate as an array or to beads or bead based technology as known in the art. Alternatively, solution based expression assays known in the art may also be used. The immobilized gene(s) may be in the form of polynucleotides that are unique or otherwise specific to the gene(s) such that the polynucleotide would be capable of hybridizing to a DNA or RNA corresponding to the gene(s). These polynucleotides may be the full length of the gene(s) or be short sequences of the genes that are optionally minimally interrupted (such as by mismatches or

inserted non-complementary basespairs) such that hybridization with a DNA or RNA corresponding to the gene(s) is not affected.

The immobilized gene(s) may be used to determine the state of nucleic acid samples prepared from sample breast cell(s) for which the pre-cancer or cancer status is not known or for confirmation of a status that is already assigned to the sample breast cell(s). Without limiting the invention, such a cell may be from a patient suspected of being afflicted with, or at risk of developing, breast cancer. The immobilized polynucleotide(s) need only be sufficient to specifically hybridize to the corresponding nucleic acid molecules derived from the sample. While even a single correlated gene sequence may to able to provide adequate accuracy in discriminating between two breast cancer cell stages, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more of the genes identified herein may be used as a subset capable of discriminating may be used in combination to increase the accuracy of the method. The invention specifically contemplates the selection of more than one, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more of the genes disclosed in the tables and figures herein for use as a subset in the identification of whether an unknown or suspicious breast cancer sample is normal or is in one or more stages of breast cancer. Optionally, the genes used will not include CloneID 809507, which is also known as GenBank accession number AA454563, described as an EST with high similarity to CD63 but of unknown function.

In embodiments where only one or a few genes are to be analyzed, the nucleic acid derived from the sample breast cancer cell(s) may be preferentially amplified by use of appropriate primers such that only the genes to be analyzed are amplified to reduce contaminating background signals from other genes expressed in the breast cell. Alternatively, and where multiple genes are to be analyzed or where very few cells (or one cell) is used, the nucleic acid from the sample may be globally amplified before hybridization to the immobilized

polynucleotides. Of course RNA, or the cDNA counterpart thereof may be directly labeled and used, without amplification, by methods known in the art.

The above assay embodiments may be used in a number of different ways to identify or detect the breast cancer stage, if any, of a breast cancer cell sample from a patient. In many cases, this would reflect a secondary screen for the patient, who may have already undergone mammography or physical exam as a primary screen. If positive, the subsequent needle biopsy, ductal lavage, fine needle aspiration, or other analogous methods may provide the sample for use in the above assay embodiments. The present invention is particularly useful in combination with non-invasive protocols, such as ductal lavage or fine needle aspiration, to prepare a breast cell sample. The current analysis of ductal lavage samples is by cytological examination by a trained pathologist who classifies the samples in terms that are at least partly subjective: unsatisfactory (too few cells), benign (including fibrocystic change), atypical (or mild atypia), suspicious (or marked atypia), or malignant.

The present invention provides a more objective set of criteria, in the form of gene expression profiles of a discrete set of genes, to discriminate (or delineate) between meaningful stages (or classes) of breast cancer cells. In particularly preferred embodiments of the invention, the assays are used to discriminate between ADH and DCIS or otherwise malignant cells, which is a critical determination for decisions concerning subsequent treatment and therapy for the patient. Another particularly preferred determination is between the three grades (I, II, III) of carcinomas *in situ* as well as the discrimination between grade III carcinomas *in situ* and invasive carcinomas. Other pairwise comparisons that are provided by the invention include, but are not limited to, normal versus ADH, normal versus carcinoma *in situ*, normal versus invasive, normal versus cancerous (i.e. carcinoma present), ADH versus cancerous, and carcinoma *in situ* versus invasive. With the use of alternative algorithms, such as neural networks, comparisons that discriminate between multiple (more than pairwise) classes may also be performed. It is believed by the inventors that the present invention is the first example of objective, molecular criteria for making these discriminations.

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In one embodiment of the invention, the isolation and analysis of a breast cancer cell sample may be performed as follows:

(1) Ductal lavage or other non-invasive procedure is performed on a patient to obtain a sample.

(2) Sample is prepared and coated onto a microscope slide. Note that ductal lavage results in clusters of cells that are cytologically examined as stated above.

(3) Pathologist or image analysis software scans the sample for the presence of atypical cells.

(4) If atypical cells are observed, those cells are harvested (e.g. by microdissection such as LCM).

(5) RNA is extracted from the harvested cells.

(6) RNA is purified, amplified, and labeled.

(7) Labeled nucleic acid is contacted with a microarray containing polynucleotides of the genes identified herein as correlated to discriminations between two or more stages of breast cancer under hybridization conditions, then processed and scanned to obtain a pattern of intensities of each spot (relative to a control for general gene expression in cells) which determine the level of expression of the gene(s) in the cells.

(8) The pattern of intensities is analyzed by comparison to the expression patterns of the genes in known samples of normal and breast cancer cells (relative to the same control).

A specific example of the above method would be performing ductal lavage following a primary screen, observing and collecting atypical cells for analysis. The comparison to known expression patterns, such as that made possible by a model generated by an algorithm (such as, but not limited to nearest neighbor type analysis, SVM, or neural networks) with reference gene expression data for the different breast cancer stages, identifies the cells as being most likely ADH.

Alternatively, the sample may permit the collection of both normal and atypical cells for analysis. The gene expression patterns for each of these two samples will be compared to each

other as well as the model and the normal versus individual abnormal comparisons therein based upon the reference data set. This approach can be significantly more powerful that the atypical cells only approach because it utilizes significantly more information from the normal cells and the differences between normal and atypical cells (in both the sample and reference data sets) to determine the status of the atypical cells from the sample.

By appropriate selection of the genes used in the analysis, identification of the relative amounts of atypical cells may also be possible, although in most clinical settings, the identification of the highest grade of breast cancer with confidence makes identification of lower grades less important. Stated differently, the identification of invasive cancer determines the clinical situation regardless of the presence of carcinoma *in situ* or hyperplastic cells, or the identification of carcinoma *in situ* makes determines the clinical situation regardless of the presence of hyperplastic cells.

With use of the present invention, skilled physicians may prescribe treatments based on non-invasive samples that they would have prescribed for a patient which had previously received a diagnosis via a solid tissue biopsy.

The above discussion is also applicable where a palpable lesion is detected followed by fine needle aspiration or needle biopsy of cells from the breast. The cells are plated and reviewed by a pathologist or automated imaging system which selects cells for analysis as described above. This again provides a means of linking visual to molecular cytology and provides a less subjective means of identifying the physiological state of breast cancer cells without the need for invasive solid tissue biopsies.

The present invention may also be used, however, with solid tissue biopsies. For example, a solid biopsy may be collected and prepared for visualization followed by determination of expression of one or more genes identified herein to determine the stage of breast cancer, if any. One preferred means is by use of *in situ* hybridization with polynucleotide or protein identifying probe(s) for assaying expression of said gene(s).

In an alternative method, the solid tissue biopsy may be used to extract molecules followed by analysis for expression of one or more gene(s). This provides the possibility of leaving out the need for visualization and collection of only those cells suspected of being atypical. This method may of course be modified such that only cells suspected of being atypical are collected and used to extract molecules for analysis. This would require visualization and selection as an prerequisite to gene expression analysis.

In a further modification of the above, both normal cells and cells suspected of being atypical are collected and used to extract molecules for analysis of gene expression. The approach, benefits and results are as described above using non-invasive sampling.

In a further alternative to all of the above, the gene(s) identified herein may be used as part of a simple PCR or array based assay simply to determine the presence of atypical cells in a sample from a non-invasive sampling procedure. This is simple to perform and utilizes genes identified to be the best discriminators of normal versus abnormal cells without the need for any cytological examination. If no atypical cells are identified, no cytological examination is necessary. If atypical cells are identified, cytological examination follows, and a more comprehensive analysis, as described above, may follow.

The genes identified herein may be used to generate a model capable of predicting the breast cancer stage (if any) of an unknown breast cell sample based on the expression of the identified genes in the sample. Such a model may be generated by any of the algorithms described herein or otherwise known in the art as well as those recognized as equivalent in the art using gene(s) (and subsets thereof) disclosed herein for the identification of whether an unknown or suspicious breast cancer sample is normal or is in one or more stages of breast cancer. The model provides a means for comparing expression profiles of gene(s) of the subset from the sample against the profiles of reference data used to build the model. The model can compare the sample profile against each of the reference profiles or against model defining delineations made based upon the reference profiles. Additionally, relative values from the sample profile may be used in comparison with the model or reference profiles.

In a preferred embodiment of the invention, breast cell samples identified as normal and abnormal (atypical) from the same subject may be analyzed for their expression profiles of the genes used to generate the model. This provides an advantageous means of identifying the stage of the abnormal sample based on relative differences from the expression profile of the normal sample. These differences can then be used in comparison to differences between normal and individual abnormal reference data which was also used to generate the model.

The detection of gene expression from the samples may be by use of a single microarray able to assay gene expression from all pairwise comparisons disclosed herein for convenience and accuracy.

Other uses of the present invention include providing the ability to identify breast cancer cell samples as being those of a particular stage of cancer for further research or study. This provides a particular advantage in many contexts requiring the identification of breast cancer stage based on objective genetic or molecular criteria rather than cytological observation. It is of particular utility to distinguish different grades of a particular breast cancer stage for further study, research or characterization because no objective criteria for such delineation was previously available.

The materials for use in the methods of the present invention are ideally suited for preparation of kits produced in accordance with well known procedures. The invention thus provides kits comprising agents for the detection of expression of the disclosed genes for identifying breast cancer stage. Such kits optionally comprising the agent with an identifying description or label or instructions relating to their use in the methods of the present invention, is provided. Such a kit may comprise containers, each with one or more of the various reagents (typically in concentrated form) utilized in the methods, including, for example, pre-fabricated microarrays, buffers, the appropriate nucleotide triphosphates (e.g., dATP, dCTP, dGTP and dTTP; or rATP, rCTP, rGTP and UTP), reverse transcriptase, DNA polymerase, RNA polymerase, and one or more primer complexes of the present invention (e.g., appropriate length

poly(T) or random primers linked to a promoter reactive with the RNA polymerase). A set of instructions will also typically be included.

The methods provided by the present invention may also be automated in whole or in part. All aspects of the present invention may also be practiced such that they consist essentially of a subset of the disclosed genes to the exclusion of material irrelevant to the identification of breast cancer stages in a cell containing sample.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

EXAMPLES

Example I: Materials and Methods

Clinical specimens

Clinical biopsies from 30 patients were obtained from the Massachusetts General Hospital with Institutional Review Board approval. The tissue from one of the patients was not associated with breast cancer of any kind since it was from a breast reduction procedure. Pathological and histological information for the biopsies were also obtained. Three independent captures of about 1000 breast epithelial cells of one or more of the four different disease stages (normal, N; atypical ductal hyperplasia, ADH; ductal carcinoma *in situ*, DCIS; invasive ductal carcinoma, IDC) were procured from each biopsy using Laser Capture Microdissection (LCM, Arcturus Engineering). Three independent captures of LCIS (lobular carcinoma in situ) in one biopsy were also made. Total RNA was extracted from the captured (procured) cells and amplified with a T7-promoter based RNA amplification protocol. The human universal

reference RNA (Stratagene, La Jolla), was similarly amplified and used as the reference channel in a two-color microarray hybridization.

Microarrays

To maximize coverage of breast cancer-related genes on the microarrays used, 11,435 cDNA clones from the IMAGE consortium (Research Genetics) were obtained. These clones were selected based on literature knowledge (such as, but not limited to, preferential expression in cancer versus normal cells) and after mining (such as, but not limited to, preferential expression in breast tissues) gene expression information in the expressed sequence tags (EST) databases and the Serial Analysis of Gene Expression (SAGE) data sets available from the National Center for Biotechnology Information (NCBI, http://www/ncbi.nlm.nih.gov).

Microarray data processing

Microarray images were analyzed with ImaGene (BioDiscovery) to find and quantitate each spot on the microarray. Spots flagged by ImaGene as poor spots using standard criteria used with the software for the standardization of signals were excluded from further analysis. Raw Cy5 (sample channel) and Cy3 (reference channel) intensities and associated local background estimates for each spot were then examined. The signal/noise ratio, defined as the spot intensity over background intensity, was used as the second criteria for spot exclusion; spots with signal/noise ratio < 3.0 in the reference channel or < 1.5 in the sample channel were excluded from further analysis. Background-subtracted intensities across the chip were normalized to the 75th-percentile of the spot intensity distribution on the entire chip (alternative normalizations to the mean, median or other point may also be used as known in the art). Cy5/Cy3 ratios of each spot for each cellular state were averaged across each of six measurements (3 LCM captures x 2 chips/capture = 6 chips); outliers among the 6 data points were removed before taking the average. The resulting data were formatted as a data matrix

(samples along the top horizontal axis and gene identity along the vertical axis) for data mining (see Figure 1 with data).

Microarray data analysis

Before further analysis, each value in a row (gene) of the gene expression matrix was divided by the median value for the row, and the resulting matrix log-transformed. Normalized, median-centered, and log-transformed, gene expression data matrix was loaded into GeneMaths software (Applied-Maths, Belgium). Clustering and discriminant analysis were performed to identify sets of genes associated with different cellular states. For each pair-wise comparison between two breast cancer stages, samples are assigned to either the positive group or negative group, and genes were sorted by their discriminatory weights. The absolute value of the weight of a gene indicates the extent of difference in expression between the two groups; the positively signed genes are expressed higher in one group and the negatively singed genes are expressed higher in the other group.

The utility of the top-ranking genes as a diagnostic test was evaluated using the support vector machines (SVMs) algorithm (see Yeang, C. H., S. Ramaswamy, et al. (2001). "Molecular classification of multiple tumor types." Bioinformatics 17 Suppl 1: S316-22; Xiong, M., X. Fang, et al. (2001). "Biomarker identification by feature wrappers." Genome Res 11(11): 1878-87**this one used linear discriminate analysis, logistic regression and svm**; Furey, T. S., N. Cristianini, et al. (2000). "Support vector machine classification and validation of cancer tissue samples using microarray expression data." Bioinformatics 16(10): 906-14; and Brown, M. P., W. N. Grundy, et al. (2000). "Knowledge-based analysis of microarray gene expression data by using support vector machines." Proc Natl Acad Sci U S A 97(1): 262-7, who state "SVMs are considered a supervised computer learning method because they exploit prior knowledge of gene function to identify unknown genes of similar function from expression data. SVMs avoid several problems associated with unsupervised clustering methods, such as hierarchical

clustering and self-organizing maps.") Other algorithms, such as, but not limited to, linear discriminate analysis, logistic regression, cluster analysis, K-th nearest neighbor, or neural nets.

The support vector machines algorithm finds the maximal margin hyperplane that separate the two groups under comparison. The method of leave-one-out cross-validation was used to test the performance of a given set of genes; one sample was taken in turn out of the training set and a model is built using the rest of the training set, which is in then applied to classify the left-out sample. The accuracy of the genes in the cross-validation procedure is the percentage of correct classifications over the total number of the training samples.

Example II: 10 Genes for discriminating between ADH and DCIS

Based upon the methodology of Example I above, 10 genes identified as capable of discriminating between ADH and DCIS are listed in Table 1 below along with a brief description of the gene. CloneID as used in the context of the present invention refers to the IMAGE Consortium clone ID number of each gene, the sequences of which are hereby incorporated by reference in their entireties as they are available from the Consortium at http://image.llnl.gov/ as accessed on the filing date of the present application. Weight refers to the absolute value indicating the extent of difference in expression between ADH and DCIS where the positively signed values are expressed higher in ADH and the negatively signed values are expressed higher in DCIS; Chromosome Location refers to the human chromosome to which the gene has been assigned, and Description provides a brief identifier of what the gene encodes. The actual data corresponding to the assigned weights are shown in Figure 2.

Table 1

GeneID	Weight	Chromosome Location	Description
825470	0.9946555	17q21-q22	topoisomerase (DNA) II alpha (170kD)
595213	0.9884884	8	hypothetical protein
796694	0.9852686	17q25	baculoviral IAP repeat-containing 5 (survivin)
1404774	-1.5638738	12p12.1-p11.2	parathyroid hormone-like hormone
823871	-1.5260464	7	SPARC-like 1 (mast9, hevin)
1882697	-1.401878	17q22-q23	peanut (Drosophila)-like 2
140071	-1.3881954	2	frizzled-related protein
160192	-1.2551663	5	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
796542	-1.1401853	3q28	ets variant gene 5 (ets-related molecule)
611532	-1.1227597	11p15.5	troponin I, skeletal, fast

Example III: Genes for discriminating between normal and non-normal (a combination of ADH, DCIS, and IDC) cells from breast tissue

As shown in Table 2 below, 850 genes were identified as being able to discriminate between normal and "abnormal" (defined in this instance as any sample that was not normal), which includes ADH, DCIS and IDC.

Table 2

CloneID	Weight	Description
1323448	1.5470535	cysteine-rich protein 1 (intestinal)
788654	1.4818381	growth factor receptor-bound protein 2
35147	1.3764654	"ESTs, Weakly similar to unnamed protein product [H.sapiens]"
745606	1.3470375	hypothetical protein PP591
1500000	1.3204029	"H2B histone family, member B"
595037	1.3057353	retinoic acid induced 3

565319   1.2369212   Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DKFZp564B1264)

122077   1.2356703   putative membrane protein

1609836   1.2349106   glutamate-ammonia ligase (glutamine synthase)

1505038   1.2292506   hypothetical protein FLJ20171

178805   1.2225746   "Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to Drosophila Scratch (Scrt), Slug and Xenopus Snail, a novel gene similar to Drosophila CG6762, STSs, GSSs and five CpG

812238   1.2132886   hypothetical protein MGC4692

1492238   1.1991653   HSPC003 protein

366132   1.1911439   "succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD"

796469   1.1850928   HSPC150 protein similar to ubiquitin-conjugating enzyme

488964   1.1545223   "H2A histone family, member O"

471568   1.1466811   hematological and neurological expressed 1

1554549   1.1440029   hydroxyacyl glutathione hydrolase

283919   1.118257   "H2A histone family, member L"

1492463   1.087152   "selenoprotein X, 1"

199403   1.082569   "lectin, galactoside-binding, soluble, 8 (galectin 8)"

796723   1.0724133   Homo sapiens clone CDABP0014 mRNA sequence

138189   1.0692241   Wolfram syndrome 1 (wolframin)

1574058   1.0651351   "1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)"

811774   1.0617336   CGI-49 protein

359887   1.052326   translocase of inner mitochondrial membrane 17 (yeast) homolog A

1709791   1.0378948   BAI1-associated protein 1

244801   1.0162794   Rho guanine exchange factor (GEF) 11

1917941   0.9960315   purine-rich element binding protein B

1858892   0.9897362   hypothetical protein MGC4825

288999   0.9896012   small protein effector 1 of Cdc42

503215	0.9757636	pilin-like transcription factor
1911343	0.967716	"RAB26, member RAS oncogene family"
2029173	0.9672743	"ESTs, Weakly similar to N-WASP [H.sapiens]"
470061	0.9665514	seven in absentia (Drosophila) homolog 2
2016908	0.9615102	"ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]"
1469425	0.9610542	SRY (sex determining region Y)-box 22
814054	0.958989	KIAA0040 gene product
814528	0.9569471	"Homo sapiens cDNA: FLJ22139 fis, clone HEP20959"
68636	0.9562688	hypothetical protein MGC2477
290841	0.9562201	"H2B histone family, member A"
236034	0.9534619	"uncoupling protein 2 (mitochondrial, proton carrier)"
782428	0.9524489	KIAA0250 gene product
131094	0.9518372	"Homo sapiens cDNA: FLJ21587 fis, clone COL06946"
488202	0.9501137	"ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]"
1435862	0.9500093	"antigen identified by monoclonal antibodies 12E7, F21 and O13"
823598	0.9452282	"proteasome (prosome, macropain) 26S subunit, non-ATPase, 12"
1492426	0.9397097	chromosome 19 open reading frame 3
795185	0.9295627	xenotropic and polytropic retrovirus receptor
810558	0.9227709	"proteasome (prosome, macropain) 26S subunit, ATPase, 4"
469686	0.9203022	"Ric (Drosophila)-like, expressed in many tissues"
280375	0.9155003	PRO2000 protein
729975	0.9149894	meningioma expressed antigen 5 (hyaluronidase)
810124	0.9124035	"platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)"
813281	0.9107661	WW domain-containing protein 1
39884	0.9091807	IMP (inosine monophosphate) dehydrogenase 1
76605	0.9028609	nesca protein
1636092	0.8997881	hypothetical protein FLJ20657

741474	0.8925439	glucose phosphate isomerase
1605426	0.8909868	hypothetical protein FLJ13352
788654	0.8886269	
868128	0.8873517	JM4 protein
308466	0.8803492	GTP-binding protein Sara
44292	0.8732235	Homo sapiens mRNA; cDNA DKFZp434C107 (from clone DKFZp434C107)
826256	0.8700831	transmembrane 7 superfamily member 1 (upregulated in kidney)
685516	0.8694652	putative G protein-coupled receptor
810711	0.869424	stearoyl-CoA desaturase (delta-9-desaturase)
753299	0.8679015	hypothetical protein FLJ10504
731044	0.8657953	glutaredoxin 2
824052	0.8650616	chromosome 6 open reading frame 1
843195	0.86501	phosphoserine phosphatase
292770	0.8570995	"Homo sapiens, clone IMAGE:3627860, mRNA, partial cds"
859761	0.8563964	poliovirus receptor-related 2 (herpesvirus entry mediator B)
347373	0.8555396	"transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)"
1640821	0.8544081	"ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]"
704414	0.8520508	small nuclear ribonucleoprotein polypeptides B and B1
810725	0.8510425	"ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD"
782608	0.8507815	mitochondrial ribosomal protein L9
2019223	0.849044	mitochondrial ribosomal protein L17
2110511	0.8471736	artemin
1474955	0.8460414	"TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)"
810612	0.842284	S100 calcium-binding protein A11 (calgizzarin)
744417	0.8409538	carnitine acetyltransferase
969877	0.8382113	"synaptosomal-associated protein, 25kD"
272529	0.8371698	phosphomannomutase 2
768570	0.8371438	hypothetical protein FLJ11280
824879	0.8366695	hypothetical protein MGC11275

2014034	0.8354357	"methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase"
2054635	0.831532	"proteasome (prosome, macropain) subunit, alpha type, 7"
2052113	0.8307595	hypothetical protein FLJ10903
742595	0.8291965	cyclin-dependent kinase 5
2016648	0.8263671	Homo sapiens mRNA; cDNA DKFZp434N1728 (from clone DKFZp434N1728)
1573251	0.823025	peroxisomal long-chain acyl-coA thioesterase
1869201	0.8202299	hypothetical protein MGC2745
37708	0.8194577	hypothetical protein MGC3101
241348	0.8182422	prenylcysteine lyase
810063	0.8168926	"growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)"
731308	0.8166873	citrate synthase
209066	0.8120797	
590774	0.8100386	mitogen-activated protein kinase 13
1435003	0.8098225	tumor suppressing subtransferable candidate 1
502774	0.8091404	hypothetical protein FLJ20623
488505	0.808712	accessory proteins BAP31/BAP29
109863	0.8066906	epithelial membrane protein 2
813419	0.8043966	"hydroxyacyl-Coenzyme A dehydrogenase, type II"
1845169	0.8033348	"RAB35, member RAS oncogene family"
742707	0.7955239	"ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]"
594500	0.7935958	EST
1456701	0.7934389	B-cell CLL/lymphoma 9
271472	0.7901735	C3HC4-like zinc finger protein
1473922	0.7892502	"actin related protein 2/3 complex, subunit 3 (21 kD)"
51773	0.7858986	hypothetical protein MGC3077
898032	0.7852733	KIAA0097 gene product
340558	0.7791736	"actin related protein 2/3 complex, subunit 5 (16 kD)"
773922	0.7767604	KIAA0005 gene product
768064	0.7743382	"cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1"

625923	0.7725056	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
150003	0.77183	hypothetical protein FLJ13187
741977	0.7715372	"B-factor, properdin"
365738	0.7709456	ESTs
814350	0.7701748	insulin-degrading enzyme
2108077	0.7700354	CGI-112 protein
209066	0.7693907	serine/threonine kinase 15
564492	0.7672548	mitochondrial carrier homolog 2
366353	0.7664569	DKFZP564C186 protein
813751	0.7659116	"sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)"
781097	0.7633668	reticulon 3
233349	0.762952	hypothetical protein FLJ10761
825327	0.7622414	"Homo sapiens cDNA FLJ14105 fis, clone MAMMA1001202"
248649	0.761865	hypothetical protein FLJ13910
589232	0.7583348	hypothetical protein FLJ11506
564847	0.757516	ESTs
754628	0.7573763	ESTs
1500162	0.7571399	ESTs
1738208	0.7565056	"a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4"
842994	0.7563101	cathepsin Z
42408	0.7559848	hypothetical protein MGC4604
470124	0.7539249	RAD1 (S. pombe) homolog
809357	0.7535411	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)
624667	0.7524325	CGI-92 protein
49351	0.75115	SEX gene
46248	0.7510436	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)
686552	0.7506994	golgi phosphoprotein 1
1631735	0.7505843	"Homo sapiens, clone IMAGE:3604336, mRNA, partial cds"
1536006	0.7499887	ESTs
83363	0.748646	protein-L-isoaspartate (D-aspartate) O-methyltransferase
713782	0.7484589	a disintegrin and metalloproteinase domain 15 (metargidin)

727078	0.7472345	"Homo sapiens cDNA: FLJ23602 fis, clone LNG15735"
503889	0.7454098	hypothetical protein FLJ10656
284261	0.7445419	uncharacterized hematopoietic stem/progenitor cells protein MDS030
1473289	0.7441483	protective protein for beta-galactosidase (galactosialidosis)
49273	0.742123	"solute carrier family 27 (fatty acid transporter), member 4"
785701	0.7413837	"RAB31, member RAS oncogene family"
41569	0.7412357	hypothetical protein FLJ12650
810402	0.7407907	hypothetical protein
1456348	0.7397574	N-acetylneuraminic acid phosphate synthase; sialic acid synthase
256619	0.7395032	hydroxysteroid (17-beta) dehydrogenase 7
743589	0.7372744	"ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]"
1409509	0.7370811	"troponin T1, skeletal, slow"
122241	0.7352191	"proteasome (prosome, macropain) subunit, beta type, 2"
470099	0.7343404	HT002 protein; hypertension-related calcium-regulated gene
725454	0.7335223	CDC28 protein kinase 2
796694	0.7317383	baculoviral IAP repeat-containing 5 (survivin)
186768	0.7298378	"Homo sapiens, clone IMAGE:3604869, mRNA"
813629	0.7288266	YME1 (S.cerevisiae)-like 1
842980	0.7284256	developmentally regulated GTP-binding protein 1
769921	0.726646	ubiquitin carrier protein E2-C
2322367	0.7249854	reticulon 4
951233	0.7240615	"proteasome (prosome, macropain) subunit, beta type, 3"
842825	0.7235007	G1 to S phase transition 1
782608	0.7230962	
2043167	0.7224903	BCL2-associated athanogene 3
827171	0.7211896	ESTs
120271	0.7208543	hypothetical protein MGC4692
1518890	0.7206844	"metallothionein-like 5, testis-specific (tesmin)"
60565	0.720547	lethal giant larvae (Drosophila) homolog 2

2050827	0.7156518	"proteasome (prosome, macropain) 26S subunit, ATPase, 5"
1635681	0.7152705	"NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)"
731023	0.7151176	WD repeat domain 5
1518402	0.7150061	KIAA1361 protein
752631	0.7139862	"fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)"
785616	0.7131593	"signal sequence receptor, alpha (translocon-associated protein alpha)"
686172	0.7131363	KIAA0008 gene product
40173	0.7124913	KIAA0807 protein
123441	0.7124698	ribosomal protein L7a
123614	0.7117834	hypothetical protein MGC4675
811024	0.7117211	bone marrow stromal cell antigen 2
2302099	0.7117055	sialidase 3 (membrane sialidase)
756442	0.7115925	P450 (cytochrome) oxidoreductase
811585	0.7087617	huntingtin (Huntington disease)
279970	0.7040135	adenosine A2a receptor
1517171	0.7036866	"interleukin 2 receptor, alpha"
838366	0.702617	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)
809944	0.7021108	KIAA0310 gene product
1393018	0.701717	"general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD)"
725978	0.7010756	"ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]"
325606	0.7008219	hypothetical protein MGC14353
795256	0.6974866	NPD007 protein
365358	0.696963	pM5 protein
67765	0.6967324	carboxypeptidase M
358267	0.6962436	"EST, Moderately similar to AF119917 63 PRO2831 [H.sapiens]"
149355	0.6943923	translocating chain-associating membrane protein
212542	0.6938079	"Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321"
79520	0.6919579	"RAB2, member RAS oncogene family"

739126 0.6881663 tissue specific transplantation antigen P35B

202514 0.6872212 DNA (cytosine-5-)-methyltransferase 3 alpha

1884404 0.6864546 KIAA0285 gene product

814378 0.6857148 "serine protease inhibitor, Kunitz type, 2"

2018337 0.6828744 "glucosidase, beta; acid (includes glucosylceramidase)"

701751 0.6824676 cut (Drosophila)-like 1 (CCAAT displacement protein)

2018084 0.6822251 Ste-20 related kinase

781019 0.6819736 paraoxonase 2

2244196 0.6807351 B-cell receptor-associated protein BAP29

124447 0.679866 KIAA1184 protein

789012 0.6794432 fibulin 2

490778 0.6788304 low molecular mass ubiquinone-binding protein (9.5kD)

2011515 0.6774452 DKFZP586B0923 protein

80764 0.6765616 hypothetical protein

841679 0.6762195 calcium and integrin binding protein (DNA-dependent protein kinase interacting protein)

108425 0.6761526

878406 0.6750777 metaxin 1

487733 0.6745496

625693 0.6744622 hypothetical protein MGC10911

1325816 0.6742078 polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)

278531 0.6737637 cytochrome c oxidase subunit VIc

744374 0.6732551 putative ankyrin-repeat containing protein

203003 0.6724027 "non-metastatic cells 4, protein expressed in"

564981 0.6712134 ESTs

812994 0.671102 "retinoid X receptor, alpha"

172517 0.6701228 hippocalcin-like 1

205049 0.6682666 protein kinase H11; small stress protein-like protein HSP22

1734309 0.6672454 sperm associated antigen 4

1631699 0.6665952 valosin-containing protein

2028949 0.6662774 hypothetical protein PRO1855

530197	0.6659784	"ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]"
199645	0.6654138	nicastrin
704254	0.6653635	a disintegrin and metalloproteinase domain 8
1592715	0.6637095	"Homer, neuronal immediate early gene, 3"
302031	0.6626629	Ste20-related serine/threonine kinase
239568	0.661735	annexin A9
770785	0.6613519	"1,2-alpha-mannosidase IC"
785795	0.660789	hypothetical protein FLJ12910
810734	0.6603412	"polymerase (DNA-directed), delta 4"
1696757	0.6591801	hypothetical protein KIAA1165
811761	0.6587469	Nijmegen breakage syndrome 1 (nibrin)
150314	0.6584621	lysophospholipase I
489351	0.65846	hypothetical protein DKFZp566J2046
593431	0.6578268	"ESTs, Moderately similar to CEGT_HUMAN CERAMIDE GLUCOSYLTRANSFERASE [H.sapiens]"
37554	0.6574292	hypothetical protein FLJ22353
126851	0.6559601	hypothetical protein FLJ11160
265103	0.6548137	Homo sapiens mRNA; cDNA DKFZp547M123 (from clone DKFZp547M123)
51083	0.6544472	"catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)"
431505	0.6534315	"ESTs, Highly similar to A31026 probable membrane receptor protein [H.sapiens]"
1420370	0.6531171	biliverdin reductase B (flavin reductase (NADPH))
1476053	0.6522237	RAD51 (S. cerevisiae) homolog (E coli RecA homolog)
882484	0.6521026	"chaperonin containing TCP1, subunit 7 (eta)"
51532	0.6504769	ADP-ribosylation factor-like 6 interacting protein
280249	0.6503028	Kruppel-like factor 7 (ubiquitous)
138788	0.6497728	prolactin receptor
1492468	0.647846	DEME-6 protein

221295	0.6477514	"inhibitor of DNA binding 2, dominant negative helix-loop-helix protein"
897806	0.6470379	"hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)"
358936	0.6441198	"ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]"
840865	0.644011	"myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)"
788334	0.6427785	mitochondrial ribosomal protein L23
366067	0.6416356	cerebellar degeneration-related protein (62kD)
825585	0.6413235	tubulin-specific chaperone e
1460110	0.6397172	"proteasome (prosome, macropain) subunit, beta type, 5"
344091	0.6381862	ESTs
196189	0.6338517	cytochrome b-5
2248488	0.6337488	ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate)
509823	0.6334191	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
144880	0.6332999	hypothetical protein from EUROIMAGE 1759349
755599	0.6330221	interferon induced transmembrane protein 1 (9-27)
207288	0.632639	insulin induced gene 1
1639531	0.6315732	"RAB27A, member RAS oncogene family"
144740	0.630134	similar to phosphatidylcholine transfer protein 2
814306	0.630078	tumor protein D52
301122	0.6299499	extracellular matrix protein 1
124298	0.6294358	microsomal glutathione S-transferase 3
1733262	0.6293971	BLu protein
376875	0.6286902	flavin containing monooxygenase 1
773188	0.6270494	"nuclear receptor subfamily 1, group D, member 2"
756666	0.6269882	"protein phosphatase 1, catalytic subunit, alpha isoform"
810156	0.6266313	deoxythymidylate kinase (thymidylate kinase)
2015517	0.6259564	hypothetical protein FLJ22237

770845	0.6253839	hexokinase 1
813707	0.6252347	regulator of G-protein signalling 16
611443	0.6244565	myoglobin
124331	0.624455	"cleavage and polyadenylation specific factor 5, 25 kD subunit"
855800	0.6235647	prolyl endopeptidase
625234	0.62188	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
753378	0.6218232	hypothetical protein FLJ22649 similar to signal peptidase SPC22/23
2055807	0.6216372	protein kinase domains containing protein similar to phosphoprotein C8FW
840878	0.6216124	seladin-1
1700436	0.6215741	ESTs
261472	0.6215341	putative nuclear protein ORF1-FL49
121251	0.6209436	hypothetical protein MGC5576
140289	0.6205892	hypothetical protein
2018821	0.6205344	ATPase inhibitor precursor
770766	0.6193342	DKFZP564C1940 protein
767798	0.6192232	"ATX1 (antioxidant protein 1, yeast) homolog 1"
845363	0.617901	"non-metastatic cells 1, protein (NM23A) expressed in"
120749	0.6172281	"ESTs, Moderately similar to KIAA1215 protein [H.sapiens]"
358162	0.616765	protein predicted by clone 23627
781342	0.6159353	hypothetical protein MGC11115
767761	0.6142782	DKFZP434B168 protein
191904	0.6141265	"BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog"
726699	0.6131491	"ESTs, Weakly similar to AAB47496 NG5 [H.sapiens]"
2326057	0.61263	MLN51 protein
784140	0.6102245	WD repeat domain 15
770355	0.6099761	"lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)"
81336	0.6099072	uteroglobin
757328	0.6097389	hypothetical protein FLJ22678
773674	0.6095732	oncogene TC21
289978	0.6090234	ubiquitin-like 4
66535	0.6088919	ornithine decarboxylase antizyme 2

826363	0.6087183	lysophospholipase II
1758590	0.6074571	"fatty-acid-Coenzyme A ligase, long-chain 3"
1553306	0.6066787	"proteasome (prosome, macropain) 26S subunit, non-ATPase, 11"
785766	0.6058332	hypothetical protein
725841	0.6051304	KIAA0662 gene product
2020898	0.6044163	"procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3"
504308	0.6041122	hypothetical protein FLJ10540
510575	0.6040713	hypothetical protein FLJ22087
49630	0.6027878	"calcium channel, voltage-dependent, L type, alpha 1D subunit"
142586	0.602037	MCT-1 protein
725284	0.6014099	"phosphorylase kinase, gamma 2 (testis)"
429799	0.6012713	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
1474424	0.6006702	"Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328"
784105	0.6003082	ESTs
2018527	0.599584	dolichyl-phosphate mannosyltransferase polypeptide 3
855563	0.5987092	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
823574	0.5978052	endosulfine alpha
323693	0.5975785	"adaptor-related protein complex 1, sigma 1 subunit"
824962	0.595868	"karyopherin alpha 2 (RAG cohort 1, importin alpha 1)"
773426	0.5941568	KIAA0391 gene product
772925	0.5940171	HSPCO34 protein
1656062	0.593408	coagulation factor XII (Hageman factor)
825740	0.5931142	DKFZp434J1813 protein
376516	0.5906248	cell division cycle 4-like
292213	0.5883092	"guanine nucleotide binding protein (G protein), beta polypeptide 2"
1898619	0.5880791	hypothetical protein MGC15737
414992	0.587733	K562 cell-derived leucine-zipper-like protein 1
1573946	0.5875624	programmed cell death 9
739109	0.5874334	"adaptor-related protein complex 2, sigma 1 subunit"

430235	0.585372	"H2B histone family, member Q"
2572170	0.5852444	"ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans [C.elegans]"
487733-2	0.5844776	"NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)"
1698036	0.5843382	ubiquitin-conjugating enzyme E2 variant 1
127646	0.5838788	
346696	0.5838269	TEA domain family member 4
74738	0.5835427	"Homo sapiens, clone IMAGE:3535294, mRNA, partial cds"
124781	0.5832065	squalene epoxidase
1883028	0.5828007	Homo sapiens mRNA; cDNA DKFZp434J1912 (from clone DKFZp434J1912)
183200	0.5801312	fumarylacetoacetate hydrolase (fumarylacetoacetase)
51741	0.5795151	GTP-binding protein
590759	0.5791873	sterol-C4-methyl oxidase-like
755301	0.5790795	"protein kinase C, delta"
843054	0.5776102	KIAA1533 protein
595213	0.5775511	hypothetical protein
752643	0.5774681	group XII secreted phospholipase A2
141852	0.5762886	"purinergic receptor P2Y, G-protein coupled, 2"
813631	0.5754418	seven transmembrane protein TM7SF3
1601947	0.5744444	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
51657	0.5736969	hypothetical protein ET
814209	0.5736866	ESTs
72050	0.5722845	"chloride channel, nucleotide-sensitive, 1A"
1635665	0.5714089	"Homo sapiens, RIKEN cDNA 2010100O12 gene, clone MGC:14813 IMAGE:4133274, mRNA, complete cds"
66406	0.5706229	hypothetical protein DKFZp762E1312
530310	0.5686743	KIAA0143 protein
41356	0.5683316	"protein phosphatase 2, regulatory subunit B (B56), alpha isoform"
1844765	0.5670398	Homo sapiens mRNA; cDNA DKFZp564O1763 (from clone DKFZp564O1763)

489823	0.5666593	"COX17 (yeast) homolog, cytochrome c oxidase assembly protein"
1517749	0.5665848	ESTs
813410	0.5664086	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)
1416782	0.5657017	"creatine kinase, brain"
1422338	0.5652946	ribonucleotide reductase M2 polypeptide
250313	0.5649247	ESTs
235986	0.5649127	"wingless-type MMTV integration site family, member 11"
66317	0.5648355	"H1 histone family, member 2"
279720	0.5645072	"ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]"
884498	0.5640535	uncharacterized hypothalamus protein HT012
503851	0.564048	nuclear receptor co-repressor/HDAC3 complex subunit
823930	0.5633774	"actin related protein 2/3 complex, subunit 1A (41 kD)"
120271	0.5626611	hypothetical protein MGC4692
782513	0.5625811	"interferon, alpha-inducible protein (clone IFI-6-16)"
246800	0.5625675	hypothetical protein FLJ10803
2309073	0.5617024	frizzled (Drosophila) homolog 5
784150	0.5598483	"RAB31, member RAS oncogene family"
139835	0.5590106	UDP-glucose dehydrogenase
1641894	0.5587185	EST
796757	0.5585876	"adaptor-related protein complex 3, sigma 1 subunit"
813616	0.5574238	FK506-binding protein like
2549634	0.5572052	activator of S phase kinase
741769	0.5565863	"polymerase (DNA directed), beta"
488642	0.5560728	"ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]"
795498	0.5557245	putative transmembrane protein
1492780	0.5555908	"Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409"
241043	0.5545302	"Human clone 137308 mRNA, partial cds"
295986	0.5544422	emopamil-binding protein (sterol isomerase)
839682	0.5542571	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)

PATENT

1581941	0.5537015	hypothetical protein FLJ14540
809466	0.5532437	DNA segment on chromosome 19 (unique) 1177 expressed sequence
1947381	0.5524634	hypothetical protein FLJ22329
825470	0.5523318	topoisomerase (DNA) II alpha (170kD)
1848977	0.5519913	glycerol kinase
700792	0.5493223	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
825386	0.5487104	"ATP synthase, H+ transporting, mitochondrial F1F0, subunit d"
826194	0.5486839	synaptotagmin-like 2
299815	0.5485843	hypothetical protein DC42
1753497	0.5485231	ovo (Drosophila) homolog-like 1
744944	0.5482368	myosin VI
1499828	0.5479012	"fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)"
415102	0.5465851	cell division cycle 25C
813387	0.5460577	diaphorase (NADH/NADPH) (cytochrome b-5 reductase)
786265	0.5443881	KIAA0750 gene product
1591264	0.5440944	transaldolase 1
756595	0.5433619	"S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))"
855749	0.5432466	triosephosphate isomerase 1
470092	0.5429717	like-glycosyltransferase
244764	0.5424555	B7 homolog 3
1637282	0.542121	hexokinase 2
417801	0.5414761	mitochondrial ribosomal protein L27
826077	0.5405591	pyruvate dehydrogenase (lipoamide) beta
757489	0.5386267	"tubulin, alpha 2"
327635	0.5368033	adenylate kinase 1
343731	0.5365018	
786067	0.5361882	cell division cycle 25B
2017415	0.5353408	centromere protein A (17kD)
292996	0.5341429	"tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide"
815781	0.5340254	heat shock 105kD
346942	0.5326646	"phosphatidylinositol glycan, class Q"

823694	0.5321203	"Homo sapiens chromosome 19, BAC CIT-HSPC_204F22 (BC228680), complete sequence; contains bacterial insertion element"
139354	0.5318709	hypothetical protein
221499	0.5317861	KIAA0508 protein
263727	0.5313082	"DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis"
489594	0.5308806	hypothetical protein FLJ11565
824524	0.5296138	UDP-galactose transporter related
951216	0.5291832	"NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)"
841260	0.5285587	hypothetical protein
283739	0.5276555	"Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838"
49117	0.5274035	KIAA0215 gene product
1762111	0.5272967	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
358609	0.5266332	NADH dehydrogenase (ubiquinone) flavoprotein 3 (10kD)
884425	0.5265114	"chaperonin containing TCP1, subunit 5 (epsilon)"
795401	0.5264278	diacylglycerol O-acyltransferase (mouse) homolog
811907	0.5246416	hypothetical protein FLJ22056
1631747	0.5245873	male-enhanced antigen
365060	0.5244569	"RAB11A, member RAS oncogene family"
743220	0.5242028	hypothetical protein FLJ12517
705064	0.5238148	"transforming, acidic coiled-coil containing protein 3"
768452	0.5237494	"Homo sapiens EST from clone 491476, full insert"
743977	0.5237158	Homo sapiens mRNA for TL132
1568825	0.5205165	Arg/Abl-interacting protein ArgBP2
772898	0.520392	ribosomal protein S15a
366834	0.5191005	envoplakin
1616253	0.5190257	breast carcinoma amplified sequence 1
322617	0.5188645	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)
825296	0.5178447	low density lipoprotein receptor defect C complementing

491524   0.5175752   mitochondrial ribosomal protein L13
143426   0.5173212   "ras homolog gene family, member B"
73009   0.516678   "ESTs, Weakly similar to A43932 mucin 2 precursor,
                      intestinal [H.sapiens]"
293569   0.5162069   chromosome 1 open reading frame 21
296702   0.5162041   "deiodinase, iodothyronine, type I"
773286   0.5158979   "solute carrier family 9 (sodium/hydrogen exchanger),
                      isoform 3 regulatory factor 1"
726658   0.5157542   "non-metastatic cells 3, protein expressed in"

753897   0.5153412   autocrine motility factor receptor
293727   0.5153298   hypothetical protein MGC861
810947   0.5151346   "LIS1-interacting protein NUDE1, rat homolog"

491465   0.5150527   hypothetical protein FLJ10035
814899   0.5142481   BCL2/adenovirus E1B 19kD-interacting protein 3-like

266500   0.5135558   ESTs
1159963 0.5133656   interferon regulatory factor 7
785707   0.5133005   protein regulator of cytokinesis 1
346134   0.5132068   calcium-regulated heat-stable protein (24kD)

486110   0.5127183   profilin 2
2017403 0.5117711   regulator of G-protein signalling 3
491527   0.5116183   "Homo sapiens, Similar to CG7083 gene product, clone
                      MGC:10534 IMAGE:3957147, mRNA, complete cds"

769600   0.5106262   uracil-DNA glycosylase 2
1558233 0.5101529   ESTs
649084   0.5099122   carbonic anhydrase XI
825822   0.5097808   hypothetical protein
1461477 0.509331   Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone
                      DKFZp586I0324)

327506   0.5092192   Homo sapiens mRNA full length insert cDNA clone
                      EUROIMAGE 327506
769942   0.509086   kinesin-like 4
505289   0.5080495   "angiotensin II, type I receptor-associated protein"

726439   0.5080059   CGI-143 protein
79726   0.5078677   "ESTs, Highly similar to T46395 hypothetical protein
                      DKFZp434I1120.1 [H.sapiens]"

810762	0.5072899	SNARE protein
785793	0.5072717	"capping protein (actin filament) muscle Z-line, alpha 1"
81599	0.5067033	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)
294397	0.5066683	DKFZP586A0522 protein
1947647	0.5064941	CGI-147 protein
795805	0.5064099	KIAA0332 protein
810959	0.505619	Rho GDP dissociation inhibitor (GDI) alpha
2322223	0.5047814	small nuclear ribonucleoprotein polypeptide A
472103	0.503987	"soc-2 (suppressor of clear, C.elegans) homolog"
810609	0.5036493	hypothetical protein PP1226
897813	0.5034689	polyadenylate binding protein-interacting protein 1
1500542	0.5032679	regulator of G-protein signalling 11
839746	0.5031787	"Homo sapiens, Similar to RIKEN cDNA 5830420C20 gene, clone IMAGE:3633379, mRNA, partial cds"
343607	0.5029133	AD-015 protein
649977	0.5002695	Homo sapiens clone CDABP0014 mRNA sequence
823940	0.4997308	"transducer of ERBB2, 1"
2250839	0.4994848	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
731080	0.4979864	hypothetical protein FLJ12661
753400	0.496254	CGI-204 protein
869375	0.4958886	"isocitrate dehydrogenase 2 (NADP+), mitochondrial"
154610	0.4948571	dynactin 4
130835	0.4946783	"Homo sapiens, Similar to clone FLB3816, clone IMAGE:3454380, mRNA"
859228	0.4942316	"isocitrate dehydrogenase 1 (NADP+), soluble"
41698	0.4938629	progesterone binding protein
30170	0.4936252	"caspase 3, apoptosis-related cysteine protease"
266218	0.4934791	hypothetical protein FLJ11350

509588	0.49319	"TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD"
1916575	0.4923447	BCL2-interacting killer (apoptosis-inducing)
744994	0.4916322	hypothetical protein FLJ12242
487444	0.4887966	"cyclic AMP phosphoprotein, 19 kD"
503866	0.4884193	sperm autoantigenic protein 17
814353	0.4883684	phorbol-12-myristate-13-acetate-induced protein 1
815501	0.4879053	hypothetical protein MGC2721
746163	0.4863317	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]"
347726	0.4837701	homeo box D8
897770	0.4836347	
1854539	0.4824023	GAP-associated tyrosine phosphoprotein p62 (Sam68)
41123	0.481642	"Homo sapiens, Similar to RIKEN cDNA 2210021G21 gene, clone MGC:14859 IMAGE:3621871, mRNA, complete cds"
856447	0.4816395	"interferon, gamma-inducible protein 30"
1568561	0.4808662	BCL2-like 1
744047	0.4802334	polo (Drosophia)-like kinase
290101	0.4800598	ESTs
455275	0.4788778	hypothetical protein FLJ23469
2069602	0.4786416	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)
592801	0.4785497	"serine palmitoyltransferase, long chain base subunit 2"
741891	0.4775456	"RAB2, member RAS oncogene family-like"
1434948	0.4771454	HIV TAT specific factor 1
430614	0.476288	"2,3-bisphosphoglycerate mutase"
454896	0.4760701	"DnaJ (Hsp40) homolog, subfamily A, member 2"
268946	0.4751692	WD40 protein Ciao1
1572710	0.4750848	hypothetical protein FLJ21213
626318	0.4746692	ubinuclein 1
377384	0.4746085	"nuclear receptor subfamily 2, group F, member 2"

1632252	0.474559	"complement component 1, q subcomponent, alpha polypeptide"
489444	0.4741367	hypothetical protein FLJ20211
345787	0.4734963	"highly expressed in cancer, rich in leucine heptad repeats"
767487	0.4729158	"ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1"
empty-31	0.4726918	blank
135640	0.4708685	syntaxin 3A
754653	0.4707927	"cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (Drosophila) homolog"
1557637	0.4705061	ESTs
788641	0.4703576	"adaptor-related protein complex 1, sigma 2 subunit"
810567	0.4702908	"Homo sapiens, clone MGC:3182 IMAGE:3356293, mRNA, complete cds"
366039	0.4701924	KIAA0892 protein
781047	0.4699376	budding uninhibited by benzimidazoles 1 (yeast homolog)
782688	0.4694868	"dynein, axonemal, light intermediate polypeptide"
210862	0.4692392	"acyl-Coenzyme A oxidase 1, palmitoyl"
510794	0.4691467	c-myc binding protein
121436	0.4691298	"Homo sapiens, clone MGC:4677 IMAGE:3532809, mRNA, complete cds"
325515	0.4689353	hypothetical protein FLJ10980
965223	0.4687291	"thymidine kinase 1, soluble"
1469148	0.467634	FGFR1 oncogene partner
149539	0.4671676	KIAA1700
2306987	0.4670155	secreted and transmembrane 1
122147	0.4652151	
2063982	0.4651856	"potassium channel, subfamily K, member 6 (TWIK-2)"
769890	0.4647115	nucleoside phosphorylase
1642496	0.4645092	hypothetical protein MGC11266
428582	0.4642013	hypothetical protein FLJ20296
66599	0.4639123	N-acetyltransferase 1 (arylamine N-acetyltransferase)
1565455	0.4634802	"nuclear receptor subfamily 2, group C, member 2"
810939	0.4634658	hypothetical protein FLJ22169
359723	0.4630712	mitochondrial elongation factor G

1027283	0.4628012	ESTs
1636844	0.4627748	ring finger protein 14
469151	0.4622121	"eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)"
813675	0.4614894	"Human D9 splice variant B mRNA, complete cds"
489657	0.4609514	tryptophan rich basic protein
469383	0.4607375	chromosome 8 open reading frame 1
40042	0.4604322	hypothetical protein FLJ10747
726637	0.45959	t-complex-associated-testis-expressed 1-like
811142	0.4595393	"phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)"
179212	0.4594831	"ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]"
292936	0.4593712	hypothetical protein FLJ10468
2046679	0.4579596	ESTs
810497	0.4572069	"ESTs, Weakly similar to A35363 synapsin I splice form a [H.sapiens]"
1585492	0.4571478	ESTs
782689	0.4570254	"solute carrier family 6 (neurotransmitter transporter, creatine), member 8"
774446	0.4567242	adrenomedullin
366156	0.4563893	"Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838"
725649	0.4559473	"nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4"
76362	0.4553121	"spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)"
754046	0.4550413	DNA segment on chromosome X (unique) 9879 expressed sequence
345538	0.4550133	cathepsin L
782439	0.454474	"ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e"
1537001	0.4539586	ESTs
345423	0.4538841	DKFZP564M112 protein
1702742	0.453453	"solute carrier family 7 (cationic amino acid transporter, y+ system), member 5"
825659	0.4515758	N-myc downstream regulated
1652310	0.4512689	"Homo sapiens, clone MGC:19613 IMAGE:3833049, mRNA, complete cds"

1523225	0.4511104	oncostatin M receptor
40773	0.4510289	"guanine nucleotide binding protein (G protein), alpha z polypeptide"
35626	0.4509825	"Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955"
358217	0.4507923	glypican 4
214996	0.45033	ESTs
177827	0.4500254	synaptotagmin VII
1075635	0.4495618	MLSN1- and TRP-related
810039	0.4491986	defender against cell death 1
772220	0.4475721	for protein disulfide isomerase-related
70606	0.4475592	ESTs
1692195	0.4471181	smg GDS-ASSOCIATED PROTEIN
841621	0.4466003	"ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]"
855707	0.4456433	ESTs
1455394	0.4455695	cytochrome c
85804	0.44449	hypothetical protein FLJ21918
809512	0.4442565	hypothetical protein FLJ10767
753457	0.4435792	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)
767289	0.4432685	hypothetical protein FLJ10055
565235	0.4428854	spermine synthase
611467	0.4428543	NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q reductase)
812105	0.4424976	ALL1-fused gene from chromosome 1q
1558642	0.4424721	hypothetical protein MGC2771
814989	0.4419384	"protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform"
1899312	0.4418248	ESTs
1486533	0.441804	keratin 16 (focal non-epidermolytic palmoplantar keratoderma)
1565079	0.4415966	B-cell linker
783681	0.4412503	upstream regulatory element binding protein 1
1422723	0.4411931	interferon-induced protein 35
785368	0.4411742	PDZ-binding kinase; T-cell originated protein kinase
1517595	0.4409591	KIAA0175 gene product
713862	0.4400704	ubiquitin-protein isopeptide ligase (E3)

83358	0.4397161	ESTs
81203	0.4391758	paraoxonase 3
74070	0.4390933	endosulfine alpha
2306221	0.4385881	"wingless-type MMTV integration site family, member 10B"
140635	0.4384907	ESTs
150118	0.4383146	hypothetical protein DKFZp434F054
214068	0.4383007	GATA-binding protein 3
1434905	0.4382073	homeo box B7
450301	0.4380657	mutL (E. coli) homolog 3
2027952	0.437854	hypothetical protein FLJ20297
745394	0.4374406	"Homo sapiens cDNA: FLJ23249 fis, clone COL04196"
824108	0.4369933	SCAN domain-containing 1
795543	0.4364791	thioredoxin peroxidase (antioxidant enzyme)
1592837	0.4355927	interferon induced transmembrane protein 2 (1-8D)
77533	0.435582	"inositol polyphosphate-5-phosphatase, 40kD"
1583198	0.4350835	"ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]"
84295	0.4349213	interleukin 1 receptor antagonist
770992	0.4346858	
837864	0.4345283	progestin induced protein
1909574	0.4342055	mitochondrial ribosomal protein S11
128695	0.4340119	"ESTs, Weakly similar to I38344 titin, cardiac muscle [H.sapiens]"
742581	0.433453	"Homo sapiens cDNA FLJ10366 fis, clone NT2RM2001420"
52103	0.432756	hypothetical protein FLJ23045
770675	0.4319407	"Homo sapiens cDNA: FLJ21323 fis, clone COL02374"
756373	0.4310628	Rho guanine exchange factor (GEF) 16
43977	0.4309655	KIAA0182 protein
2322079	0.4309341	
25440	0.4304195	"staufen (Drosophila, RNA-binding protein) homolog 2"
207794	0.4297389	"nuclear factor (erythroid-derived 2), 45kD"
746190	0.4291743	hypothetical protein DKFZp761B1514
74566	0.4279059	"exportin 1 (CRM1, yeast, homolog)"
76196	0.4278385	hypothetical protein FLJ20062

826173	0.4276784	profilin 1
1587863	0.4270229	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
2017721	0.4268089	"ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]"
809464	0.426456	"fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)"
41826	0.4264531	ESTs
1687976	0.4257058	"endoplasmic reticulum chaperone SIL1, homolog of yeast"
416436	0.4252319	mitochondrial ribosomal protein L24
145491	0.4250102	protocadherin 1 (cadherin-like 1)
810316	0.4245985	very long-chain acyl-CoA synthetase; lipidosin
629944	0.4242364	myosin VB
1637302	0.424164	DNAJ domain-containing
754625	0.4236648	"ATPase, Class II, type 9A"
298417	0.4235025	trefoil factor 3 (intestinal)
47853	0.4231314	"aldehyde dehydrogenase 4 family, member A1"
809727	0.4224266	unc-51 (C. elegans)-like kinase 1
774502	0.4222849	"protein tyrosine phosphatase, non-receptor type 12"
785840	0.4219115	"SEC24 (S. cerevisiae) related gene family, member D"
823907	0.4218216	hypothetical protein FLJ10511
1679942	0.4215618	KIAA1053 protein
823909	0.4215098	
1600239	0.421459	HSPC037 protein
85195	0.4207753	"growth arrest and DNA-damage-inducible, gamma"
1640282	0.4205899	KIAA1240 protein
782503	0.4205398	fatty acid desaturase 1
266312	0.4201146	"ATPase, Cu++ transporting, beta polypeptide (Wilson disease)"
884511	0.4199518	cytochrome c oxidase subunit VIIb
2051697	0.4197703	"inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta"

724888	0.4196322	"cytochrome P450, subfamily IVB, polypeptide 1"
809507	0.4189998	hypothetical protein FLJ20568
151449	0.4189856	"protein tyrosine phosphatase, non-receptor type 21"
743860	0.4189656	"hypothetical protein, clone 2746033"
345833	0.4187433	heterogeneous nuclear ribonucleoprotein A/B
259950	0.4187278	hypothetical protein FLJ14991
283751	0.4179154	cortistatin
810875	0.4176896	"solute carrier family 26, member 6"
26883	0.4176151	"protein kinase (cAMP-dependent, catalytic) inhibitor beta"
38356	0.4173012	"cytochrome P450, subfamily 46 (cholesterol 24-hydroxylase)"
35191	0.4165847	stromal cell-derived factor 2
75859	-2.4150177	N-myc downstream-regulated gene 2
1569187	-1.9090486	heparan sulfate (glucosamine) 3-O-sulfotransferase 4
345670	-1.889471	"ESTs, Moderately similar to I59348 CCAAT binding transcription factor CBF subunit C - rat [R.norvegicus]"
760299	-1.8654555	dickkopf (Xenopus laevis) homolog 3
753071	-1.8417236	"Homo sapiens cDNA: FLJ22528 fis, clone HRC12825"
344720	-1.7951928	glycophorin C (Gerbich blood group)
810002	-1.7256692	"Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds"
200814	-1.7140538	"membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)"
131839	-1.7087069	folate receptor 1 (adult)
300632	-1.6969092	hypothetical protein FLJ21044 similar to Rbig1
811920	-1.6924158	"interleukin 11 receptor, alpha"
486683	-1.6799604	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
1558675	-1.6577507	SRY (sex determining region Y)-box 10
840266	-1.6530726	"Homo sapiens cDNA: FLJ22667 fis, clone HSI08385"
285377	-1.6514168	pellino (Drosophila) homolog 2
1469377	-1.6473741	lipoma HMGIC fusion partner-like 2

45099	-1.6325981	regucalcin (senescence marker protein-30)
1161564	-1.5917197	desmuslin
298122	-1.5678888	frizzled (Drosophila) homolog 7
796542	-1.5553964	ets variant gene 5 (ets-related molecule)
289760	-1.5534789	"ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]"
22917	-1.5156635	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
838478	-1.5059801	neurocalcin delta
788234	-1.4824055	"inhibitor of DNA binding 4, dominant negative helix-loop-helix protein"
377461	-1.4787671	"caveolin 1, caveolae protein, 22kD"
67741	-1.4786722	PP2135 protein
839736	-1.4745405	"crystallin, alpha B"
712139	-1.4736508	ADP-ribosylation factor-like 7
160192	-1.4695435	"ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]"
742685	-1.4440371	disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
1556433	-1.4191955	GRO3 oncogene
1554167	-1.4126653	hypothetical protein FLJ14529
877621	-1.3987023	nGAP-like protein
1882697	-1.3873266	peanut (Drosophila)-like 2
72778	-1.3873177	"caspase 7, apoptosis-related cysteine protease"
666879	-1.3624072	annexin A8
69002	-1.3581187	PPAR(gamma) angiopoietin related protein
811848	-1.3549757	hypothetical protein
490023	-1.3516302	hypothetical protein MGC2648
781017	-1.3232108	early growth response 2 (Krox-20 (Drosophila) homolog)
767202	-1.3217103	latent transforming growth factor beta binding protein 2
291478	-1.3155899	runt-related transcription factor 3
757191	-1.2902603	ESTs
130201	-1.2885369	intercellular adhesion molecule 2
1635320	-1.2878152	"amiloride-sensitive cation channel 2, neuronal"

140574   -1.2754214   "small inducible cytokine subfamily D (Cys-X3-Cys),
member 1 (fractalkine, neurotactin)"

416676   -1.2751042   pellino (Drosophila) homolog 1
814798   -1.2748689   "aldehyde dehydrogenase 1 family, member A3"

611532   -1.273871   "troponin I, skeletal, fast"
2056139   -1.2697411   LIM domain protein
377275   -1.2665702   ataxia-telangiectasia group D-associated protein

303109   -1.2557454   purinergic receptor (family A group 5)
813265   -1.2549431   Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone
DKFZp564H1916)

878836   -1.2507242   "secretory granule, neuroendocrine protein 1 (7B2 protein)"

1473471   -1.2409979   KIAA0194 protein
529843   -1.2405917   "ESTs, Moderately similar to JC5238 galactosylceramide-
like protein, GCP [H.sapiens]"

505864   -1.2393277   RalGDS-like gene
781014   -1.2359239   suppression of tumorigenicity 5
470393   -1.2354879   "matrix metalloproteinase 7 (matrilysin, uterine)"

290378   -1.2346086   podocalyxin-like
196435   -1.2282733   ESTs
71087   -1.2181178   "v-maf musculoaponeurotic fibrosarcoma (avian) oncogene
family, protein F"
34093   -1.2156885   EST
76182   -1.2102812   hypothetical protein DKFZp761F241
884462   -1.2078038   Down syndrome critical region gene 1
277571   -1.2030738   KIAA1706 protein
841308   -1.200964   "myosin, light polypeptide kinase"
162308   -1.2006293   ESTs
52419   -1.2004086   Friedreich ataxia region gene X123
488404   -1.1981268   Homo sapiens clone TUA8 Cri-du-chat region mRNA

712401   -1.193113   "phosphoinositide-3-kinase, catalytic, delta polypeptide"

289428   -1.1923798   "neurotrophic tyrosine kinase, receptor, type 2"

814443   -1.1905978   hypothetical protein MGC3232
153760   -1.1793765   EphB1

1917449	-1.1785893	"serum amyloid A4, constitutive"
1493218	-1.164886	hypothetical protein FLJ22297
843070	-1.1647509	nucleoporin 88kD
753038	-1.1629978	kinesin family member C3
811088	-1.1625002	ephrin-B3
2106144	-1.1619925	regulated in glioma
796181	-1.1584587	growth arrest-specific 6
1257131	-1.1566479	ESTs
1473274	-1.1557062	"myosin regulatory light chain 2, smooth muscle isoform"
208718	-1.1498532	annexin A1
811837	-1.1468554	eukaryotic translation elongation factor 1 alpha 1
768571	-1.1461886	SRY (sex determining region Y)-box 8
1474900	-1.1347123	keratin 15
756708	-1.1346161	"potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4"
1555924	-1.1342985	CSR1 protein
811837	-1.1269309	
1878409	-1.1144369	catechol-O-methyltransferase
786069	-1.1143906	beta-site APP-cleaving enzyme
815737	-1.1116223	"ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle"
132857	-1.0989746	Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)
1871116	-1.0975491	Homo sapiens mRNA; cDNA DKFZp434C1714 (from clone DKFZp434C1714); partial cds
133236	-1.0945253	"RNA binding motif protein, X chromosome"
283023	-1.0825166	chemokine (C-X3-C) receptor 1
2016775	-1.0761731	"G protein-coupled receptor, family C, group 5, member B"
897963	-1.0751021	phosphatidic acid phosphatase type 2A
814316	-1.0654718	ribosomal protein L13
47043	-1.0559861	tensin
625399	-1.0523138	hypothetical protein similar to beta-transducin family
416959	-1.051868	nuclear factor I/B
366100	-1.0467604	matrilin 2

753162	-1.0416438	KIAA0603 gene product
491403	-1.0411657	"tumor necrosis factor receptor superfamily, member 1B"
813256	-1.0407652	"ATP-binding cassette, sub-family B (MDR/TAP), member 1"
740620	-1.0395569	tropomyosin 2 (beta)
1577736	-1.035115	epidermal growth factor (beta-urogastrone)
70245	-1.0348655	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 50374
1626996	-1.0328113	c-fos induced growth factor (vascular endothelial growth factor D)
360254	-1.0325653	"cysteine-rich, angiogenic inducer, 61"
80344	-1.0323882	interleukin 7 receptor
530958	-1.0316423	smoothened (Drosophila) homolog
34150	-1.0302576	ESTs
809784	-1.030253	"kallikrein 6 (neurosin, zyme)"
990881	-1.0289558	
416434	-1.0284229	SCN Circadian Oscillatory Protein (SCOP)
162308	-1.023071	
796475	-1.0217348	four and a half LIM domains 3
32489	-1.0196444	hypothetical protein DKFZp566A1524
2504881	-1.0194516	signal transducer and activator of transcription 5A
188335	-1.0161259	"egf-like module containing, mucin-like, hormone receptor-like sequence 2"
593023	-1.0135883	"dystrobrevin, beta"
139660	-1.0134677	ESTs
772913	-1.0122192	calreticulin
270826	-1.0112851	"Homo sapiens cDNA FLJ13329 fis, clone OVARC1001795"
1864302	-1.0099902	E74-like factor 5 (ets domain transcription factor)
1587710	-1.0092611	period (Drosophila) homolog 1
1584540	-1.0077508	Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)
788136	-1.0073983	"phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)"
40027	-1.0057005	ESTs
1856063	-1.0036618	tweety (Drosophila) homolog 1
209537	-0.9988461	zinc finger protein 221

628955	-0.997687	forkhead box O1A (rhabdomyosarcoma)
2095066	-0.9972552	"alcohol dehydrogenase 1C (class I), gamma polypeptide"
1636166	-0.9969091	KIAA0668 protein
882248	-0.9965858	transgelin
415816	-0.9954308	ESTs
897731	-0.9927981	latrophilin
868396	-0.9916319	"tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide"
343760	-0.9907562	SH3 domain binding glutamic acid-rich protein like 2
1572298	-0.9906095	"CD3Z antigen, zeta polypeptide (TiT3 complex)"
1474337	-0.986117	"phosphorylase, glycogen; brain"
1609665	-0.9851713	BarH-like homeobox 2
2243051	-0.9835274	kallikrein 8 (neuropsin/ovasin)
27544	-0.9834143	prominin (mouse)-like 1
281190	-0.9830533	ESTs
161456	-0.9820939	serum amyloid A1
505243	-0.980381	"inositol 1,4,5-triphosphate receptor, type 2"

Example IV: Genes for discriminating between normal and ADH

As shown in Table 3 below, 600 genes were identified as being able to discriminate between normal and ADH.

Table 3

CloneID	Weight	Description
1323448	1.3237504	cysteine-rich protein 1 (intestinal)
594500	1.158305	EST
824052	1.034408	chromosome 6 open reading frame 1
149539	0.9878366	KIAA1700
788654	0.9585887	growth factor receptor-bound protein 2
1517749	0.947675	ESTs
1492238	0.9155471	HSPC003 protein

366353	0.9154768	DKFZP564C186 protein
1609836	0.898716	glutamate-ammonia ligase (glutamine synthase)
138189	0.8950816	Wolfram syndrome 1 (wolframin)
344959	0.8945717	gene for serine/threonine protein kinase
1435862	0.8934643	antigen identified by monoclonal antibodies 12E7, F21 and O13
2014373	0.8820247	HNK-1 sulfotransferase
23776	0.879215	quinoid dihydropteridine reductase
293569	0.8708985	chromosome 1 open reading frame 21
130835	0.8659688	Homo sapiens, Similar to clone FLB3816, clone IMAGE:3454380, mRNA
236034	0.8541082	uncoupling protein 2 (mitochondrial, proton carrier)
488025	0.8525751	Kruppel-associated box protein
178805	0.8524069	Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to Drosophila Scratch (Scrt), Slug and Xenopus Snail, a novel gene similar to Drosophila CG6762, STSs, GSSs and five CpG
745606	0.8514931	hypothetical protein PP591
1492463	0.8378401	selenoprotein X, 1
530197	0.8206765	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
898222	0.8092364	Homo sapiens clone 24418 mRNA sequence
782608	0.8041049	mitochondrial ribosomal protein L9
450301	0.8030667	mutL (E. coli) homolog 3
196189	0.7992668	cytochrome b-5
363144	0.7924672	transcription factor AP-2 beta (activating enhancer-binding protein 2 beta)
68636	0.7904354	hypothetical protein MGC2477
795185	0.7765346	xenotropic and polytropic retrovirus receptor
255754	0.7720883	LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein
767798	0.7682106	ATX1 (antioxidant protein 1, yeast) homolog 1

1558233	0.7654043	ESTs
769600	0.763743	uracil-DNA glycosylase 2
1156538	0.7512287	potassium inwardly-rectifying channel, subfamily J, member 11
1587863	0.7507482	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
1709791	0.740832	BAI1-associated protein 1
741891	0.7360507	RAB2, member RAS oncogene family-like
788654	0.7336359	
811774	0.7223819	CGI-49 protein
1738208	0.7166687	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4
120138	0.7096046	J domain containing protein 1
2248488	0.7033736	ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate)
265103	0.702883	Homo sapiens mRNA; cDNA DKFZp547M123 (from clone DKFZp547M123)
2054122	0.698129	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3
701751	0.6961443	cut (Drosophila)-like 1 (CCAAT displacement protein)
811582	0.690137	golgi phosphoprotein 2
266312	0.6856592	ATPase, Cu++ transporting, beta polypeptide (Wilson disease)
35147	0.6842172	ESTs, Weakly similar to unnamed protein product [H.sapiens]
1325816	0.6829962	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)
358217	0.6801945	glypican 4
233349	0.6764709	hypothetical protein FLJ10761
741977	0.6758385	B-factor, properdin
145132	0.6725186	mannose-P-dolichol utilization defect 1
33267	0.6679827	
279720	0.6607182	ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]
565319	0.6603668	Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DKFZp564B1264)
771173	0.6594128	mitochondrial ribosomal protein S21

271472   0.6582514   C3HC4-like zinc finger protein
768570   0.6581316   hypothetical protein FLJ11280
744417   0.6563238   carnitine acetyltransferase
826256   0.6554059   transmembrane 7 superfamily member 1 (upregulated in kidney)

2250839   0.654954   androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)

179212   0.6499845   ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]

785701   0.6496359   RAB31, member RAS oncogene family
186768   0.6495706   Homo sapiens, clone IMAGE:3604869, mRNA

503215   0.6457259   pilin-like transcription factor
37554   0.6440792   hypothetical protein FLJ22353
2710524   0.6399293   nuclear receptor coactivator 3
284261   0.6398576   uncharacterized hematopoietic stem/progenitor cells protein MDS030
741769   0.6390692   polymerase (DNA directed), beta
743146   0.6388187   hypothetical protein FLJ23403
814528   0.6329458   Homo sapiens cDNA: FLJ22139 fis, clone HEP20959

742595   0.6324947   cyclin-dependent kinase 5
810063   0.630827   growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
590310   0.6299822   Homo sapiens mRNA; cDNA DKFZp434E2321 (from clone DKFZp434E2321); partial cds

841679   0.6283163   calcium and integrin binding protein (DNA-dependent protein kinase interacting protein)

131094   0.6268883   Homo sapiens cDNA: FLJ21587 fis, clone COL06946

788334   0.6264069   mitochondrial ribosomal protein L23
1574058   0.6261947   1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)

731308   0.6259858   citrate synthase
826194   0.6205287   synaptotagmin-like 2
2110511   0.6203153   artemin
811907   0.6180993   hypothetical protein FLJ22056

814350	0.6173648	insulin-degrading enzyme
611443	0.6112713	myoglobin
782608	0.6105794	
22778	0.6100322	sulfortranferase family 4A, member 1
128695	0.608873	ESTs, Weakly similar to I38344 titin, cardiac muscle [H.sapiens]
47853	0.6077928	aldehyde dehydrogenase 4 family, member A1
814209	0.6076904	ESTs
590774	0.6071935	mitogen-activated protein kinase 13
969877	0.6064355	synaptosomal-associated protein, 25kD
1469425	0.6055267	SRY (sex determining region Y)-box 22
301122	0.6041028	extracellular matrix protein 1
199403	0.6027193	lectin, galactoside-binding, soluble, 8 (galectin 8)
813845	0.6018909	RNA, U transporter 1
810331	0.6014164	quiescin Q6
770766	0.600234	DKFZP564C1940 protein
279970	0.5992634	adenosine A2a receptor
490778	0.5957445	low molecular mass ubiquinone-binding protein (9.5kD)
288999	0.5955672	small protein effector 1 of Cdc42
504959	0.5953946	Homo sapiens mRNA; cDNA DKFZp586G0321 (from clone DKFZp586G0321)
42408	0.5930231	hypothetical protein MGC4604
263727	0.5926363	DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis
854763	0.5918867	Homo sapiens cDNA FLJ11341 fis, clone PLACE1010786
729975	0.5908615	meningioma expressed antigen 5 (hyaluronidase)
1733262	0.5891897	BLu protein
730313	0.5887579	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
1500000	0.5871787	H2B histone family, member B
595037	0.5870709	retinoic acid induced 3
1635681	0.5859113	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)
2325804	0.5840656	95 kDa retinoblastoma protein binding protein
2014856	0.5837779	major histocompatibility complex, class I-like sequence

40173	0.5771304	KIAA0807 protein
796723	0.576028	Homo sapiens clone CDABP0014 mRNA sequence
239568	0.5750382	annexin A9
2018527	0.5732092	dolichyl-phosphate mannosyltransferase polypeptide 3
1649374	0.5731982	homogentisate 1,2-dioxygenase (homogentisate oxidase)
809357	0.571929	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)
366132	0.5711651	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
83358	0.5709886	ESTs
1762111	0.5703701	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
244801	0.5693836	Rho guanine exchange factor (GEF) 11
127646	0.5663395	
39884	0.5659552	IMP (inosine monophosphate) dehydrogenase 1
202577	0.5629317	histamine N-methyltransferase
588262	0.5614929	Homo sapiens, Similar to RIKEN cDNA 2600001A11 gene, clone MGC:9907 IMAGE:3870073, mRNA, complete cds
813419	0.5602324	hydroxyacyl-Coenzyme A dehydrogenase, type II
1911343	0.559091	RAB26, member RAS oncogene family
859761	0.5582503	poliovirus receptor-related 2 (herpesvirus entry mediator B)
342181	0.557997	B-cell CLL/lymphoma 2
1558108	0.5577768	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
2017403	0.5568495	regulator of G-protein signalling 3
122394	0.5554851	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
824879	0.5548666	hypothetical protein MGC11275
1708055	0.554593	glioblastoma overexpressed
1456701	0.5545861	B-cell CLL/lymphoma 9
186301	0.5537115	Homo sapiens cDNA FLJ12924 fis, clone NT2RP2004709
126851	0.5535041	hypothetical protein FLJ11160
826622	0.5532463	KIAA0430 gene product

151449	0.5503739	protein tyrosine phosphatase, non-receptor type 21
826668	0.550158	KIAA0274 gene product
76605	0.5482232	nesca protein
786072	0.5450231	myosin IC
2244196	0.5432772	B-cell receptor-associated protein BAP29
704414	0.5431136	small nuclear ribonucleoprotein polypeptides B and B1
739578	0.5402953	GPI-anchored metastasis-associated protein homolog
1404774	0.5399447	parathyroid hormone-like hormone
66599	0.5399379	N-acetyltransferase 1 (arylamine N-acetyltransferase)
359250	0.5382989	carbonic anhydrase IV
488202	0.5378254	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]
235986	0.5371486	wingless-type MMTV integration site family, member 11
214068	0.5357344	GATA-binding protein 3
1500542	0.5341753	regulator of G-protein signalling 11
470092	0.5319336	like-glycosyltransferase
589115	0.531314	matrix metalloproteinase 1 (interstitial collagenase)
810734	0.5308572	polymerase (DNA-directed), delta 4
685516	0.5304998	putative G protein-coupled receptor
171912	0.5297738	Homo sapiens cDNA FLJ10960 fis, clone PLACE1000564
1858892	0.5295858	hypothetical protein MGC4825
414992	0.5293379	K562 cell-derived leucine-zipper-like protein 1
37708	0.5283276	hypothetical protein MGC3101
713782	0.5273402	a disintegrin and metalloproteinase domain 15 (metargidin)
471568	0.5255851	hematological and neurological expressed 1
812238	0.5237287	hypothetical protein MGC4692
1631735	0.5228778	Homo sapiens, clone IMAGE:3604336, mRNA, partial cds
74070	0.5225238	endosulfine alpha
782497	0.5218113	Homo sapiens, clone IMAGE:3010666, mRNA, partial cds
502774	0.5204735	hypothetical protein FLJ20623

1517171	0.5204242	interleukin 2 receptor, alpha
50562	0.5195335	chromosome 8 open reading frame 4
60565	0.5192032	lethal giant larvae (Drosophila) homolog 2
1641894	0.5187462	EST
51083	0.5170561	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)
296702	0.5164562	deiodinase, iodothyronine, type I
2018337	0.5163293	glucosidase, beta; acid (includes glucosylceramidase)
1605426	0.5150013	hypothetical protein FLJ13352
1474149	0.5138729	poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)
26294	0.5137265	RNB6
810017	0.5135433	plasminogen activator, urokinase receptor
825822	0.5134094	hypothetical protein
810725	0.51329	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD
781019	0.5132896	paraoxonase 2
726658	0.5132765	non-metastatic cells 3, protein expressed in
1916575	0.5127478	BCL2-interacting killer (apoptosis-inducing)
1469148	0.5125351	FGFR1 oncogene partner
726703	0.5118991	Homo sapiens clone 23736 mRNA sequence
725978	0.5108817	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
1573946	0.509585	programmed cell death 9
51741	0.5094912	GTP-binding protein
156363	0.5086284	hypothetical protein FLJ12934
177827	0.5085582	synaptotagmin VII
294397	0.505999	DKFZP586A0522 protein
826077	0.503983	pyruvate dehydrogenase (lipoamide) beta
949938	0.5011384	cystatin C (amyloid angiopathy and cerebral hemorrhage)
1957136	0.5006732	phenylethanolamine N-methyltransferase
2018084	0.4999242	Ste-20 related kinase
784140	0.4984039	WD repeat domain 15
810981	0.498146	hypothetical protein FLJ20699

627248	0.4972176	SBBI31 protein
2302099	0.4967769	sialidase 3 (membrane sialidase)
302031	0.49677	Ste20-related serine/threonine kinase
183440	0.4967506	arylsulfatase A
1609748	0.4955206	hypothetical protein MGC10882
183200	0.4955056	fumarylacetoacetate hydrolase (fumarylacetoacetase)
2306697	0.4953741	neuromedin B
292770	0.4944242	Homo sapiens, clone IMAGE:3627860, mRNA, partial cds
856447	0.494183	interferon, gamma-inducible protein 30
855563	0.4941473	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
839081	0.4939384	homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2
49273	0.4937997	solute carrier family 27 (fatty acid transporter), member 4
289505	0.4933344	ESTs, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]
782689	0.4930071	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
767495	0.4922026	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)
782537	0.490998	Homo sapiens cDNA: FLJ22562 fis, clone HSI01814
855029	0.4904632	Ac-like transposable element
705274	0.4904221	diacylglycerol kinase, delta (130kD)
202514	0.4902228	DNA (cytosine-5-)-methyltransferase 3 alpha
725649	0.4878638	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
1884404	0.4878341	KIAA0285 gene product
825296	0.4858551	low density lipoprotein receptor defect C complementing
839580	0.4826315	ESTs
289857	0.4823282	phenylethanolamine N-methyltransferase
491465	0.4821169	hypothetical protein FLJ10035
360778	0.4820033	
261472	0.4814013	putative nuclear protein ORF1-FL49
840768	0.4812559	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD

123614	0.4800042	hypothetical protein MGC4675
1603583	0.4785029	SH3 domain binding glutamic acid-rich protein like
782688	0.4780253	dynein, axonemal, light intermediate polypeptide
784150	0.4763599	RAB31, member RAS oncogene family
770869	0.4762758	hypothetical protein MGC2592
455269	0.4761389	
365358	0.4756564	pM5 protein
795256	0.4753832	NPD007 protein
756666	0.474441	protein phosphatase 1, catalytic subunit, alpha isoform
767706	0.4731085	ESTs
488505	0.4727394	accessory proteins BAP31/BAP29
344073	0.4726399	ESTs, Weakly similar to K1CI_HUMAN KERATIN, TYPE I CYTOSKELETAL 9 [H.sapiens]
1558151	0.4723511	basic leucine zipper transcription factor, ATF-like
823615	0.471739	Homo sapiens cDNA: FLJ21245 fis, clone COL01184
49351	0.4697521	SEX gene
1541711	0.4694413	Homo sapiens cDNA: FLJ21513 fis, clone COL05778
868652	0.4682053	complement component 4B
430318	0.4681908	parvalbumin
143426	0.4679928	ras homolog gene family, member B
951125	0.4675003	peroxisomal D3,D2-enoyl-CoA isomerase
66535	0.466705	ornithine decarboxylase antizyme 2
813281	0.4659334	WW domain-containing protein 1
726699	0.4658249	ESTs, Weakly similar to AAB47496 NG5 [H.sapiens]
1492468	0.4643107	DEME-6 protein
1492426	0.4635224	chromosome 19 open reading frame 3
489106	0.4628623	hypothetical protein FLJ11210
488422	0.4626549	high-mobility group 20B
278430	0.4612914	kinesin family member 5C
1518890	0.4610867	metallothionein-like 5, testis-specific (tesmin)
2017756	0.4608709	homolog of yeast MOG1
813631	0.4607567	seven transmembrane protein TM7SF3
1557637	0.4588694	ESTs
298417	0.4587501	trefoil factor 3 (intestinal)

810402	0.4583168	hypothetical protein
767761	0.4565666	DKFZP434B168 protein
1473289	0.4540707	protective protein for beta-galactosidase (galactosialidosis)
773142	0.4530754	hypothetical protein MGC2827
1652310	0.4525789	Homo sapiens, clone MGC:19613 IMAGE:3833049, mRNA, complete cds
812143	0.4519186	fibronectin leucine rich transmembrane protein 3
2326057	0.4506179	MLN51 protein
1075635	0.4502629	MLSN1- and TRP-related
825327	0.4497029	Homo sapiens cDNA FLJ14105 fis, clone MAMMA1001202
809838	0.4466933	
786545	0.4453714	protein phosphatase 1, regulatory (inhibitor) subunit 3B
183556	0.4452493	gap junction protein, alpha 4, 37kD (connexin 37)
503889	0.4433034	hypothetical protein FLJ10656
725321	0.44288	estrogen receptor 1
731459	0.4427978	Homo sapiens cDNA: FLJ22296 fis, clone HRC04468
752631	0.4426961	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
1558642	0.4426424	hypothetical protein MGC2771
120271	0.4425879	hypothetical protein MGC4692
487932	0.4419815	synaptotagmin-like 2
1592715	0.4417898	Homer, neuronal immediate early gene, 3
308466	0.4417728	GTP-binding protein Sara
840882	0.441569	nucleotide binding protein
823727	0.4406546	Homo sapiens, clone IMAGE:2905978, mRNA, partial cds
1636092	0.4404649	hypothetical protein FLJ20657
1505038	0.43988	hypothetical protein FLJ20171
490965	0.4389746	ESTs
346696	0.437234	TEA domain family member 4
345032	0.4360992	ESTs
487733	0.4356439	
810612	0.4352602	S100 calcium-binding protein A11 (calgizzarin)
122077	0.434495	putative membrane protein
417801	0.4325892	mitochondrial ribosomal protein L27

878406	0.4311455	metaxin 1
1947381	0.4311314	hypothetical protein FLJ22329
232789	0.4292025	polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)
809944	0.4291762	KIAA0310 gene product
2019101	0.4289318	angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8)
1656062	0.4288838	coagulation factor XII (Hageman factor)
1390584	0.4284863	mitochondrial intermediate peptidase
1693357	0.4274493	endothelin 2
75859	-1.6337267	N-myc downstream-regulated gene 2
1558675	-1.4515145	SRY (sex determining region Y)-box 10
753071	-1.4473398	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
810002	-1.2720931	Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds
712139	-1.2371074	ADP-ribosylation factor-like 7
815737	-1.1857965	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
503671	-1.1528584	Homo sapiens cDNA FLJ14368 fis, clone HEMBA1001122
345670	-1.135654	ESTs, Moderately similar to I59348 CCAAT binding transcription factor CBF subunit C - rat [R.norvegicus]
753038	-1.1168529	kinesin family member C3
741139	-1.1025542	eyes absent (Drosophila) homolog 2
839736	-1.1019142	crystallin, alpha B
2013178	-1.0884449	death associated transcription factor 1
1577736	-1.076549	epidermal growth factor (beta-urogastrone)
788234	-1.0610946	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
150897	-1.0221539	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
757873	-1.0188169	cyclin-dependent kinase 5, regulatory subunit 1 (p35)
291478	-1.0093382	runt-related transcription factor 3
486683	-1.0075654	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
290378	-1.0043647	podocalyxin-like
772913	-0.9823487	calreticulin

544639	-0.9767278	ESTs
814798	-0.9611553	aldehyde dehydrogenase 1 family, member A3
131839	-0.959265	folate receptor 1 (adult)
840266	-0.9425178	Homo sapiens cDNA: FLJ22667 fis, clone HSI08385
1555924	-0.9421074	CSR1 protein
756708	-0.9396531	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4
838478	-0.934433	neurocalcin delta
742562	-0.9269494	chromosome 16 open reading frame 5
1469377	-0.9086679	lipoma HMGIC fusion partner-like 2
884462	-0.9065675	Down syndrome critical region gene 1
796542	-0.9052403	ets variant gene 5 (ets-related molecule)
32493	-0.9043423	integrin, alpha 6
284592	-0.9019931	PRO1659 protein
788136	-0.8998648	phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)
1161564	-0.8865787	desmuslin
1635320	-0.8845852	amiloride-sensitive cation channel 2, neuronal
344720	-0.8822302	glycophorin C (Gerbich blood group)
1534700	-0.8804685	KIAA0830 protein
193913	-0.8724313	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
71087	-0.870641	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F
300632	-0.8586688	hypothetical protein FLJ21044 similar to Rbig1
416676	-0.8568853	pellino (Drosophila) homolog 1
69002	-0.8528453	PPAR(gamma) angiopoietin related protein
742685	-0.852598	disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
140574	-0.8498606	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)
23831	-0.8493217	aldolase C, fructose-bisphosphate
470393	-0.848482	matrix metalloproteinase 7 (matrilysin, uterine)
1474337	-0.844539	phosphorylase, glycogen; brain

753301	-0.8393651	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)
51078	-0.8348835	ribosomal protein L44
3172883	-0.8293392	ESTs, Weakly similar to 1709359A dopamine D4 receptor [H.sapiens]
877621	-0.8289253	nGAP-like protein
811920	-0.8286379	interleukin 11 receptor, alpha
156211	-0.8269263	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 1 (Renal tubular acidosis with deafness)
760299	-0.8251086	dickkopf (Xenopus laevis) homolog 3
285377	-0.8214706	pellino (Drosophila) homolog 2
345034	-0.8161772	small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)
298122	-0.8158372	frizzled (Drosophila) homolog 7
842896	-0.8123068	hypothetical protein DKFZp762L0311
843070	-0.8071984	nucleoporin 88kD
1257131	-0.8069059	ESTs
796539	-0.803124	KRAB-associated protein 1
139660	-0.79833	ESTs
666879	-0.7950485	annexin A8
200814	-0.7920988	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
2016775	-0.7914834	G protein-coupled receptor, family C, group 5, member B
1946448	-0.790849	caveolin 2
1473471	-0.7906678	KIAA0194 protein
1556433	-0.7877792	GRO3 oncogene
1636156	-0.7827089	hypothetical protein FLJ21709
40299	-0.78007	growth differentiation factor 10
1636166	-0.7788972	KIAA0668 protein
1609665	-0.7765472	BarH-like homeobox 2
250797	-0.7739669	hypothetical protein FLJ20038
220395	-0.7687195	hypothetical protein FLJ23293 similar to ARL-6 interacting protein-2
208718	-0.7660278	annexin A1
41869	-0.7646494	hypothetical protein FLJ11017
490023	-0.7621736	hypothetical protein MGC2648
1607229	-0.7562938	tumor protein D52-like 1
133236	-0.7561129	RNA binding motif protein, X chromosome

785733 -0.7554682 hypothetical protein FLJ12892
32489 -0.7521767 hypothetical protein DKFZp566A1524
70201 -0.7513314 mitochondrial solute carrier
611481 -0.7507264 HMG-box transcription factor TCF-3
1554167 -0.7503289 hypothetical protein FLJ14529
768571 -0.7476813 SRY (sex determining region Y)-box 8
783698 -0.7411614 lipin 1
341759 -0.7393558 lung type-I cell membrane-associated glycoprotein

665384 -0.7388404 KIAA1609 protein
142259 -0.7380151 tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcrption factor IIIA-interacting protein

810057 -0.7363941 vasoactive intestinal peptide receptor 1
27544 -0.7342174 prominin (mouse)-like 1
739193 -0.7338774 cellular retinoic acid-binding protein 1
813256 -0.7334866 ATP-binding cassette, sub-family B (MDR/TAP), member 1

293964 -0.7275302 butyrophilin, subfamily 3, member A1
272706 -0.7274769 alpha2,3-sialyltransferase
209537 -0.7245778 zinc finger protein 221
67741 -0.7229251 PP2135 protein
823714 -0.7215045 nuclear receptor co-repressor/HDAC3 complex subunit

471196 -0.7192752 integral membrane protein 3
813265 -0.7192289 Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)

42681 -0.718704 NY-REN-25 antigen
1601845 -0.7178673 Ca2+-promoted Ras inactivator
725152 -0.7173869 hypothetical protein DKFZp762A227
22917 -0.7173328 Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)

703541 -0.7118124 KIAA1858 protein
529843 -0.7117107 ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]

377461 -0.7093974 caveolin 1, caveolae protein, 22kD
1569187 -0.7091259 heparan sulfate (glucosamine) 3-O-sulfotransferase 4

1456118	-0.7074166	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)
289760	-0.7058375	ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]
341774	-0.7044768	major histocompatibility complex, class I, A
75078	-0.7028415	ESTs
505864	-0.7020337	RalGDS-like gene
415191	-0.700303	KIAA0161 gene product
188335	-0.7002579	egf-like module containing, mucin-like, hormone receptor-like sequence 2
132711	-0.6985643	Kruppel-like factor 5 (intestinal)
1864302	-0.6943806	E74-like factor 5 (ets domain transcription factor)
344854	-0.692296	ankyrin repeat domain 3
454970	-0.6853932	DKFZP434G032 protein
79629	-0.6849525	
767068	-0.6819032	DKFZP586G1517 protein
378813	-0.679848	secretory leukocyte protease inhibitor (antileukoproteinase)
725076	-0.6798005	5'-nucleotidase (purine), cytosolic type B
491403	-0.6760814	tumor necrosis factor receptor superfamily, member 1B
43764	-0.6743049	hypothetical protein FLJ14033 similar to hypoxia inducible factor 3, alpha subunit
725622	-0.6731681	ESTs
431231	-0.6692022	EGF-containing fibulin-like extracellular matrix protein 2
488956	-0.6682156	CUG triplet repeat, RNA-binding protein 2
72778	-0.6614808	caspase 7, apoptosis-related cysteine protease
360254	-0.6612871	cysteine-rich, angiogenic inducer, 61
76182	-0.6603322	hypothetical protein DKFZp761F241
773487	-0.6598647	hypothetical protein MGC3032
162308	-0.6580605	ESTs
283023	-0.6577611	chemokine (C-X3-C) receptor 1
196992	-0.6573113	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
303109	-0.6571713	purinergic receptor (family A group 5)
897731	-0.6548064	latrophilin

289428   -0.6542789 neurotrophic tyrosine kinase, receptor, type 2

196435   -0.653913   ESTs
504791   -0.6537859 glutathione S-transferase A4
812975   -0.6527728 KIAA0172 protein
488404   -0.6521658 Homo sapiens clone TUA8 Cri-du-chat region mRNA

345056   -0.6490368 KIAA1404 protein
786069   -0.6484842 beta-site APP-cleaving enzyme
48518   -0.6455041 ATP-binding cassette, sub-family A (ABC1), member 5

812048   -0.6438062 prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)

868396   -0.6426678 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide

70245   -0.6422928 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 50374
40027   -0.6418674 ESTs
840944   -0.6399619 early growth response 1
809784   -0.6348991 kallikrein 6 (neurosin, zyme)
1881774   -0.6332545 KIAA1678
52419   -0.6326767 Friedreich ataxia region gene X123
120106   -0.631375   caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
725680   -0.6295778 transcription factor AP-2 gamma (activating enhancer-binding protein 2 gamma)

1493218   -0.6292715 hypothetical protein FLJ22297
2018423   -0.6275903 death-associated protein kinase 2
1486082   -0.6241275 heparin-binding growth factor binding protein

868169   -0.6224058 lipoprotein lipase
209137   -0.6161588 gamma-aminobutyric acid (GABA) A receptor, epsilon

248886   -0.6161134 rab3 GTPase-activating protein, non-catalytic subunit (150kD)

73252   -0.6115602 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)

612274   -0.6108452 tubulin, alpha 1 (testis specific)
346545   -0.6098367 laminin, beta 1
84464   -0.6091345 hypothetical protein FLJ12806

628955 -0.6088522 forkhead box O1A (rhabdomyosarcoma)
490414 -0.6078858 chromosome 2 open reading frame 2
752837 -0.6056177 Homo sapiens mRNA for FLJ00074 protein, partial cds

796904 -0.604755 pleiomorphic adenoma gene-like 1
418159 -0.6038708 synaptogyrin 1
323238 -0.6032171 GRO1 oncogene (melanoma growth stimulating activity, alpha)

1570427 -0.601608 hypothetical protein MGC4309
1500815 -0.6008126 Homo sapiens cDNA: FLJ22130 fis, clone HEP19632

416959 -0.5999728 nuclear factor I/B
782460 -0.5988226 Homo sapiens cDNA FLJ10500 fis, clone NT2RP2000369

824602 -0.5965816 interferon, gamma-inducible protein 16
878798 -0.5956349 beta-2-microglobulin
32299 -0.5945347 inositol(myo)-1(or 4)-monophosphatase 2
277571 -0.59335 KIAA1706 protein
703964 -0.5918604 inositol polyphosphate phosphatase-like 1
796498 -0.5900328 hypothetical protein FLJ14007
504927 -0.5894078 epithelial protein up-regulated in carcinoma, membrane
        associated protein 17

813520 -0.5889772 EphB3
341763 -0.5868818 caspase 5, apoptosis-related cysteine protease

1856063 -0.5866417 tweety (Drosophila) homolog 1
825356 -0.5850287 Homo sapiens cDNA FLJ11997 fis, clone HEMBB1001458

745011 -0.5836864 Homo sapiens mRNA for KIAA1750 protein, partial cds

812256 -0.5832398 Homo sapiens cDNA: FLJ21693 fis, clone COL09609

2017960 -0.5822336 PP1201 protein
713129 -0.5822078 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated
        serine esterase 3)
815142 -0.5782827 spastic ataxia of Charlevoix-Saguenay (sacsin)

80727 -0.5766546 receptor tyrosine kinase-like orphan receptor 1

45099 -0.5753698 regucalcin (senescence marker protein-30)

415816 -0.5750184 ESTs

306798 -0.5742664 NGFI-A binding protein 1 (EGR1 binding protein 1)

563634 -0.5737239 dendritic cell protein
757191 -0.5735888 ESTs
740620 -0.5730915 tropomyosin 2 (beta)
1470048 -0.5729078 lymphocyte antigen 6 complex, locus E
788518 -0.5724497 peroxisomal membrane protein 3 (35kD, Zellweger syndrome)

177665 -0.5718286
221846 -0.5714352 checkpoint suppressor 1
37671 -0.5712258 hypothetical protein FLJ21610
2072862 -0.5694163 v-akt murine thymoma viral oncogene homolog 2

132637 -0.5694152 grancalcin, EF-hand calcium-binding protein

1474900 -0.5693091 keratin 15
34093 -0.5692081 EST
1881689 -0.568518 hypothetical protein FLJ20281
1883327 -0.5684295 ESTs
1902764 -0.5683052 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3

781017 -0.5676944 early growth response 2 (Krox-20 (Drosophila) homolog)

34150 -0.5673709 ESTs
137602 -0.5667198 Homo sapiens mRNA; cDNA DKFZp434G0972 (from clone DKFZp434G0972)

460126 -0.5652362 KIAA0819 protein
470128 -0.5652125 myosin IE
1880885 -0.5638973 ESTs
811848 -0.5637994 hypothetical protein
1417886 -0.563564 hypothetical protein FLJ23239
756847 -0.5632582 deformed epidermal autoregulatory factor 1 (Drosophila)

505243 -0.5616577 inositol 1,4,5-triphosphate receptor, type 2
840677 -0.5611985 immunoglobulin kappa constant
1911663 -0.5610314 ESTs
66491 -0.5579872 plasmolipin
1420842 -0.5574834 mucosa associated lymphoid tissue lymphoma translocation gene 1
1626996 -0.5573507 c-fos induced growth factor (vascular endothelial growth factor D)

281190	-0.5572026	ESTs
796475	-0.5563457	four and a half LIM domains 3
1870305	-0.5558155	heat shock 27kD protein 2
767456	-0.5555493	hypothetical protein FLJ22167
292388	-0.554297	
795178	-0.5532479	lactate dehydrogenase C
809998	-0.5519459	amylase, alpha 2A; pancreatic
1734754	-0.5512835	hypothetical protein B
27769	-0.5501268	ESTs
950355	-0.550114	ESTs, Weakly similar to S13495 pregnancy zone protein [H.sapiens]
144924	-0.5498123	chromosome 6 open reading frame 5
502436	-0.5489864	insulin receptor substrate 2
138672	-0.5483104	ESTs
160192	-0.5482009	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
768007	-0.547374	hypothetical protein
130201	-0.5468031	intercellular adhesion molecule 2
1587847	-0.5466442	minichromosome maintenance deficient (mis5, S. pombe) 6
1558212	-0.5458261	ESTs
1470278	-0.5449844	hypothetical protein FLJ21841
811088	-0.5445374	ephrin-B3
197056	-0.5440514	ESTs
868630	-0.5426831	transforming growth factor beta-stimulated protein TSC-22
530958	-0.5423532	smoothened (Drosophila) homolog
810097	-0.5423072	Homo sapiens cDNA: FLJ21721 fis, clone COLF0381
207735	-0.5422739	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
79254	-0.541673	MHC class I region ORF
85634	-0.5410684	complement component 1, s subcomponent
531319	-0.5404527	serine/threonine kinase 12
754028	-0.5396001	KIAA0469 gene product
470148	-0.5393193	ESTs
35828	-0.5391332	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)

970590   -0.5383645 Homo sapiens mRNA; cDNA DKFZp434A115 (from clone DKFZp434A115)

753162   -0.5377767 KIAA0603 gene product
241066   -0.5369493 Homo sapiens cDNA: FLJ21028 fis, clone CAE07155

1909935   -0.5368632 ESTs
153760   -0.5361176 EphB1
247616   -0.5358709 lipoma HMGIC fusion partner
1031640   -0.5354869 ESTs
24958   -0.5349519 Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone DKFZp434C2016)

1686766   -0.5342051 Rag D protein
2009491   -0.5334821 cyclin-E binding protein 1
611532   -0.5320107 troponin I, skeletal, fast
811149   -0.5319742 chromosome 9 open reading frame 3
844703   -0.5309356 Sam68-like phosphotyrosine protein, T-STAR

70749   -0.5295091 Homo sapiens cDNA: FLJ21874 fis, clone HEP02488

324927   -0.5284875 KIAA0375 gene product
491519   -0.5282605 Homo sapiens clone 24775 mRNA sequence

754040   -0.5282144 NS1-associated protein 1
767765   -0.5282008 GTP-binding protein overexpressed in skeletal muscle

2028722   -0.5277252 osteoblast specific factor 2 (fasciclin I-like)
509458   -0.5266016 hypothetical protein from clone 643
360518   -0.5253745 guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1

40021   -0.5240809 hairless protein (putative single zinc finger transcription factor protein, responsible for autosomal recessive universal congenital alopecia, HR gene)

1901310   -0.5229967 KIAA1209 protein
33949   -0.5222135 phosphoribosyl pyrophosphate synthetase-associated protein 1

814316   -0.521831   ribosomal protein L13
488130   -0.5201845 Homo sapiens cDNA FLJ20767 fis, clone COL06986

462939   -0.5200097 ESTs

770848 -0.5188717 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]

245296 -0.5184238 RAD52 (S. cerevisiae) homolog
753034 -0.5182019 nuclear factor I/X (CCAAT-binding transcription factor)

712829 -0.5181236 LIM domain only 2 (rhombotin-like 1)
1577920 -0.5161377 ESTs
814526 -0.5156162 seb4D
773301 -0.5147295 cadherin 3, type 1, P-cadherin (placental)
77972 -0.5144916 complement component 3
1704155 -0.5133015 hypothetical protein SBBI48
1572298 -0.5126426 CD3Z antigen, zeta polypeptide (TiT3 complex)

755689 -0.5122586 retinoic acid receptor, gamma
1876217 -0.5108977 DnaJ (Hsp40) homolog, subfamily A, member 2

712401 -0.5107426 phosphoinositide-3-kinase, catalytic, delta polypeptide

713839 -0.5088558 transcription factor AP-4 (activating enhancer-binding protein 4)

180803 -0.5083354 inositol polyphosphate-1-phosphatase
814443 -0.5075293 hypothetical protein MGC3232

Example V: Genes for discriminating between normal and DCIS

As shown in Table 4 below, 1300 genes were identified as being able to discriminate between normal and DCIS.

Table 4

CloneID	Weight	Description
1323448	1.397391	cysteine-rich protein 1 (intestinal)
788654	1.2615322	growth factor receptor-bound protein 2
1505038	1.1904802	hypothetical protein FLJ20171
745606	1.1825585	hypothetical protein PP591

565319 1.0969429 Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DKFZp564B1264)

35147 1.0886084 ESTs, Weakly similar to unnamed protein product [H.sapiens]

178805 1.0274897 Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to Drosophila Scratch (Scrt), Slug and Xenopus Snail, a novel gene similar to Drosophila CG6762, STSs, GSSs and five CpG

796469 1.0269115 HSPC150 protein similar to ubiquitin-conjugating enzyme

1609836 1.0164283 glutamate-ammonia ligase (glutamine synthase)

366132 1.013995 succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD

1500000 1.0118809 H2B histone family, member B
812238 1.0043787 hypothetical protein MGC4692
595037 0.990461 retinoic acid induced 3
1554549 0.9764206 hydroxyacyl glutathione hydrolase
488964 0.9569176 H2A histone family, member O
138189 0.9386802 Wolfram syndrome 1 (wolframin)
283919 0.937383 H2A histone family, member L
823598 0.9153521 proteasome (prosome, macropain) 26S subunit, non-ATPase, 12

810711 0.9128832 stearoyl-CoA desaturase (delta-9-desaturase)

1911343 0.9116745 RAB26, member RAS oncogene family
503215 0.9108688 pilin-like transcription factor
811774 0.9073627 CGI-49 protein
122077 0.9021901 putative membrane protein
1492238 0.9019233 HSPC003 protein
469686 0.8919992 Ric (Drosophila)-like, expressed in many tissues

685516 0.8762873 putative G protein-coupled receptor
359887 0.8692353 translocase of inner mitochondrial membrane 17 (yeast) homolog A
131094 0.8675719 Homo sapiens cDNA: FLJ21587 fis, clone COL06946

1492463 0.8634521 selenoprotein X, 1

843195	0.8603524	phosphoserine phosphatase
796723	0.8573155	Homo sapiens clone CDABP0014 mRNA sequence
488202	0.8463961	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]
1492426	0.8445255	chromosome 19 open reading frame 3
280375	0.8392836	PRO2000 protein
290841	0.8346933	H2B histone family, member A
1917941	0.8340565	purine-rich element binding protein B
1469425	0.8296141	SRY (sex determining region Y)-box 22
2016908	0.8282806	ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]
471568	0.8264546	hematological and neurological expressed 1
150003	0.8251408	hypothetical protein FLJ13187
2029173	0.8213721	ESTs, Weakly similar to N-WASP [H.sapiens]
731044	0.8169506	glutaredoxin 2
244801	0.8066357	Rho guanine exchange factor (GEF) 11
2054635	0.7914755	proteasome (prosome, macropain) subunit, alpha type, 7
1605426	0.787298	hypothetical protein FLJ13352
1709791	0.7837549	BAI1-associated protein 1
470061	0.77977	seven in absentia (Drosophila) homolog 2
1640821	0.7790286	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
199403	0.7754748	lectin, galactoside-binding, soluble, 8 (galectin 8)
741474	0.7732047	glucose phosphate isomerase
1435862	0.7697423	antigen identified by monoclonal antibodies 12E7, F21 and O13
239568	0.767277	annexin A9
841679	0.7666686	calcium and integrin binding protein (DNA-dependent protein kinase interacting protein)
729975	0.7649717	meningioma expressed antigen 5 (hyaluronidase)
2016648	0.7633048	Homo sapiens mRNA; cDNA DKFZp434N1728 (from clone DKFZp434N1728)
2052113	0.7627076	hypothetical protein FLJ10903

347373	0.7563599	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)
814054	0.7539407	KIAA0040 gene product
741977	0.7538359	B-factor, properdin
272529	0.7486269	phosphomannomutase 2
824879	0.7432221	hypothetical protein MGC11275
122241	0.7394284	proteasome (prosome, macropain) subunit, beta type, 2
744417	0.7356767	carnitine acetyltransferase
868128	0.7347171	JM4 protein
241348	0.7324115	prenylcysteine lyase
509823	0.7304507	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
1636092	0.7270017	hypothetical protein FLJ20657
42408	0.725109	hypothetical protein MGC4604
686552	0.7231319	golgi phosphoprotein 1
898032	0.7216	KIAA0097 gene product
754628	0.7195265	ESTs
826256	0.7190206	transmembrane 7 superfamily member 1 (upregulated in kidney)
2043167	0.7167431	BCL2-associated athanogene 3
827171	0.7154964	ESTs
502774	0.7148695	hypothetical protein FLJ20623
781097	0.7126945	reticulon 3
810725	0.7115051	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD
768570	0.7102463	hypothetical protein FLJ11280
813281	0.7092607	WW domain-containing protein 1
39884	0.7075527	IMP (inosine monophosphate) dehydrogenase 1
969877	0.707469	synaptosomal-associated protein, 25kD
704254	0.7061648	a disintegrin and metalloproteinase domain 8
236034	0.7039329	uncoupling protein 2 (mitochondrial, proton carrier)
782428	0.701077	KIAA0250 gene product
489351	0.7003616	hypothetical protein DKFZp566J2046
37708	0.6986007	hypothetical protein MGC3101
271472	0.6978431	C3HC4-like zinc finger protein
782608	0.6978285	mitochondrial ribosomal protein L9

704414	0.6940045	small nuclear ribonucleoprotein polypeptides B and B1
288999	0.6938843	small protein effector 1 of Cdc42
51773	0.6925666	hypothetical protein MGC3077
124447	0.6918546	KIAA1184 protein
470099	0.6915952	HT002 protein; hypertension-related calcium-regulated gene
429799	0.6915155	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
1858892	0.6904662	hypothetical protein MGC4825
796694	0.6893307	baculoviral IAP repeat-containing 5 (survivin)
284261	0.6890531	uncharacterized hematopoietic stem/progenitor cells protein MDS030
814528	0.6878182	Homo sapiens cDNA: FLJ22139 fis, clone HEP20959
788654	0.6866898	
68636	0.6838604	hypothetical protein MGC2477
308466	0.6800103	GTP-binding protein Sara
1574058	0.6796357	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
79520	0.6769129	RAB2, member RAS oncogene family
1473289	0.674396	protective protein for beta-galactosidase (galactosialidosis)
365738	0.6740773	ESTs
768064	0.673441	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1
773922	0.6730903	KIAA0005 gene product
1869201	0.6727191	hypothetical protein MGC2745
686172	0.6724684	KIAA0008 gene product
810558	0.6698194	proteasome (prosome, macropain) 26S subunit, ATPase, 4
753299	0.6694573	hypothetical protein FLJ10504
725454	0.6669973	CDC28 protein kinase 2
470124	0.6641768	RAD1 (S. pombe) homolog
2014034	0.6620303	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase
209066	0.6611038	
859761	0.6573769	poliovirus receptor-related 2 (herpesvirus entry mediator B)
589232	0.6551447	hypothetical protein FLJ11506

340558	0.6550804	actin related protein 2/3 complex, subunit 5 (16 kD)
186768	0.6550741	Homo sapiens, clone IMAGE:3604869, mRNA
813629	0.6549767	YME1 (S.cerevisiae)-like 1
1492780	0.6544659	Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409
809944	0.6530236	KIAA0310 gene product
83363	0.6526164	protein-L-isoaspartate (D-aspartate) O-methyltransferase
149355	0.6520333	translocating chain-associating membrane protein
752631	0.650399	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
785616	0.6484744	signal sequence receptor, alpha (translocon-associated protein alpha)
76605	0.6484522	nesca protein
742707	0.6476434	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]
325606	0.647638	hypothetical protein MGC14353
769921	0.6464245	ubiquitin carrier protein E2-C
1435003	0.6457486	tumor suppressing subtransferable candidate 1
1473922	0.6450042	actin related protein 2/3 complex, subunit 3 (21 kD)
1456348	0.6417276	N-acetylneuraminic acid phosphate synthase; sialic acid synthase
1500162	0.6416738	ESTs
1573251	0.6410435	peroxisomal long-chain acyl-coA thioesterase
46248	0.640944	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)
49351	0.6386132	SEX gene
824052	0.6375787	chromosome 6 open reading frame 1
1420370	0.6344209	biliverdin reductase B (flavin reductase (NADPH))
842994	0.6343858	cathepsin Z
810612	0.6341098	S100 calcium-binding protein A11 (calgizzarin)
123614	0.633308	hypothetical protein MGC4675
124781	0.6324418	squalene epoxidase
814378	0.6317382	serine protease inhibitor, Kunitz type, 2
2108077	0.6312583	CGI-112 protein

289978   0.6308861 ubiquitin-like 4
67765   0.6300886 carboxypeptidase M
742595   0.6265846 cyclin-dependent kinase 5
727078   0.6263882 Homo sapiens cDNA: FLJ23602 fis, clone LNG15735

487733   0.6262778
366067   0.625758 cerebellar degeneration-related protein (62kD)

292770   0.6231261 Homo sapiens, clone IMAGE:3627860, mRNA, partial cds

366353   0.6203012 DKFZP564C186 protein
810063   0.620086 growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
810124   0.6162712 platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)
713782   0.6149877 a disintegrin and metalloproteinase domain 15 (metargidin)

782608   0.6137782
530197   0.6122721 ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]

44292   0.6122043 Homo sapiens mRNA; cDNA DKFZp434C107 (from clone DKFZp434C107)

2018084   0.6119069 Ste-20 related kinase
789012   0.6104002 fibulin 2
256619   0.6102239 hydroxysteroid (17-beta) dehydrogenase 7
825327   0.6094796 Homo sapiens cDNA FLJ14105 fis, clone MAMMA1001202

842980   0.6081528 developmentally regulated GTP-binding protein 1

811761   0.6045809 Nijmegen breakage syndrome 1 (nibrin)
1601947   0.6045149 cytochrome c oxidase subunit VIIa polypeptide 2 (liver)

1474955   0.6045103 TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)

1758590   0.6040962 fatty-acid-Coenzyme A ligase, long-chain 3

1456701   0.6038789 B-cell CLL/lymphoma 9
207288   0.603346 insulin induced gene 1
1631699   0.6027911 valosin-containing protein

1635681	0.6022549	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)
768452	0.6018854	Homo sapiens EST from clone 491476, full insert
897806	0.6015789	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
108425	0.6008772	
770785	0.600311	1,2-alpha-mannosidase IC
2110511	0.5987863	artemin
785795	0.598504	hypothetical protein FLJ12910
120271	0.5982507	hypothetical protein MGC4692
248649	0.5975539	hypothetical protein FLJ13910
2244196	0.5972111	B-cell receptor-associated protein BAP29
66406	0.5966701	hypothetical protein DKFZp762E1312
1537001	0.59528	ESTs
2028949	0.5946445	hypothetical protein PRO1855
40173	0.5940582	KIAA0807 protein
490778	0.5932928	low molecular mass ubiquinone-binding protein (9.5kD)
503889	0.5930018	hypothetical protein FLJ10656
781019	0.5918462	paraoxonase 2
196189	0.5916252	cytochrome b-5
1734309	0.5894492	sperm associated antigen 4
814350	0.588877	insulin-degrading enzyme
2018821	0.5887114	ATPase inhibitor precursor
365358	0.5883524	pM5 protein
430235	0.5874504	H2B histone family, member Q
1422338	0.5874097	ribonucleotide reductase M2 polypeptide
770845	0.5870877	hexokinase 1
172517	0.5869599	hippocalcin-like 1
1884404	0.5849803	KIAA0285 gene product
625923	0.5839066	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
2322367	0.5832711	reticulon 4
624667	0.5828923	CGI-92 protein
826363	0.5823873	lysophospholipase II
859228	0.5817344	isocitrate dehydrogenase 1 (NADP+), soluble
2302099	0.5813788	sialidase 3 (membrane sialidase)
209066	0.5794211	serine/threonine kinase 15

1844765	0.57783	Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
191904	0.5770884	BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog
951233	0.5767874	proteasome (prosome, macropain) subunit, beta type, 3
809357	0.5767382	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)
825740	0.5762093	DKFZp434J1813 protein
51532	0.5758765	ADP-ribosylation factor-like 6 interacting protein
203003	0.5743416	non-metastatic cells 4, protein expressed in
2015517	0.5742448	hypothetical protein FLJ22237
205049	0.5734444	protein kinase H11; small stress protein-like protein HSP22
752643	0.5732323	group XII secreted phospholipase A2
753400	0.5732322	CGI-204 protein
564847	0.573202	ESTs
785766	0.5731938	hypothetical protein
825585	0.5722829	tubulin-specific chaperone e
37554	0.5706008	hypothetical protein FLJ22353
144880	0.5704416	hypothetical protein from EUROIMAGE 1759349
49273	0.5691181	solute carrier family 27 (fatty acid transporter), member 4
743589	0.568516	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]
1616253	0.567837	breast carcinoma amplified sequence 1
1581941	0.5676045	hypothetical protein FLJ14540
431505	0.5670119	ESTs, Highly similar to A31026 probable membrane receptor protein [H.sapiens]
2019223	0.5663073	mitochondrial ribosomal protein L17
840878	0.5648009	seladin-1
811024	0.5646461	bone marrow stromal cell antigen 2
564492	0.5626905	mitochondrial carrier homolog 2
725841	0.561197	KIAA0662 gene product
701751	0.561139	cut (Drosophila)-like 1 (CCAAT displacement protein)
767798	0.560181	ATX1 (antioxidant protein 1, yeast) homolog 1

109863	0.559767	epithelial membrane protein 2
1536006	0.5590182	ESTs
1845169	0.5588842	RAB35, member RAS oncogene family
343607	0.5588222	AD-015 protein
212542	0.5587394	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321
1700436	0.5569949	ESTs
795256	0.5567908	NPD007 protein
2011515	0.5566484	DKFZP586B0923 protein
504308	0.5564295	hypothetical protein FLJ10540
772925	0.5562164	HSPCO34 protein
469383	0.5558732	chromosome 8 open reading frame 1
810402	0.5555749	hypothetical protein
1409509	0.554703	troponin T1, skeletal, slow
2050827	0.5544641	proteasome (prosome, macropain) 26S subunit, ATPase, 5
770355	0.5518948	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
813410	0.5513568	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)
80764	0.5510626	hypothetical protein
1631735	0.5502891	Homo sapiens, clone IMAGE:3604336, mRNA, partial cds
625234	0.550211	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
279970	0.5502099	adenosine A2a receptor
1518402	0.5497179	KIAA1361 protein
753378	0.548977	hypothetical protein FLJ22649 similar to signal peptidase SPC22/23
594500	0.5474088	EST
590774	0.5460342	mitogen-activated protein kinase 13
2055807	0.5460123	protein kinase domains containing protein similar to phosphoprotein C8FW
773188	0.5454398	nuclear receptor subfamily 1, group D, member 2
126851	0.5454014	hypothetical protein FLJ11160
244764	0.5450377	B7 homolog 3
813419	0.5447006	hydroxyacyl-Coenzyme A dehydrogenase, type II
233349	0.5446353	hypothetical protein FLJ10761
785701	0.5446211	RAB31, member RAS oncogene family
268946	0.5440003	WD40 protein Ciao1

611443	0.5432426	myoglobin
510575	0.5430211	hypothetical protein FLJ22087
491465	0.5420241	hypothetical protein FLJ10035
1393018	0.5404243	general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD)
785840	0.5401209	SEC24 (S. cerevisiae) related gene family, member D
1460110	0.5392177	proteasome (prosome, macropain) subunit, beta type, 5
731308	0.5371204	citrate synthase
301122	0.5368073	extracellular matrix protein 1
66535	0.5363248	ornithine decarboxylase antizyme 2
265103	0.5361177	Homo sapiens mRNA; cDNA DKFZp547M123 (from clone DKFZp547M123)
788334	0.5347204	mitochondrial ribosomal protein L23
813631	0.534683	seven transmembrane protein TM7SF3
1553306	0.5344506	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
1461477	0.5343834	Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324)
199645	0.5334951	nicastrin
884425	0.5327862	chaperonin containing TCP1, subunit 5 (epsilon)
1518890	0.5314577	metallothionein-like 5, testis-specific (tesmin)
756442	0.5313744	P450 (cytochrome) oxidoreductase
2326057	0.5310995	MLN51 protein
138788	0.5302936	prolactin receptor
1698036	0.5298397	ubiquitin-conjugating enzyme E2 variant 1
811585	0.5288102	huntingtin (Huntington disease)
795185	0.5276861	xenotropic and polytropic retrovirus receptor
629944	0.5273447	myosin VB
784105	0.5259815	ESTs
1696757	0.5254296	hypothetical protein KIAA1165
139835	0.5253386	UDP-glucose dehydrogenase
1738208	0.5240868	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4

593431	0.5235073	ESTs, Moderately similar to CEGT_HUMAN CERAMIDE GLUCOSYLTRANSFERASE [H.sapiens]
2309073	0.5226599	frizzled (Drosophila) homolog 5
825470	0.5218731	topoisomerase (DNA) II alpha (170kD)
839682	0.5208954	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
1517171	0.5195255	interleukin 2 receptor, alpha
376516	0.5195127	cell division cycle 4-like
774446	0.5181672	adrenomedullin
1476053	0.5179015	RAD51 (S. cerevisiae) homolog (E coli RecA homolog)
489594	0.5178551	hypothetical protein FLJ11565
1573946	0.5173691	programmed cell death 9
503851	0.5170168	nuclear receptor co-repressor/HDAC3 complex subunit
882484	0.5165756	chaperonin containing TCP1, subunit 7 (eta)
51083	0.5162686	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)
221295	0.5157877	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
725978	0.5147267	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
796757	0.5122331	adaptor-related protein complex 3, sigma 1 subunit
150314	0.5114988	lysophospholipase I
302031	0.5111067	Ste20-related serine/threonine kinase
293569	0.5103638	chromosome 1 open reading frame 21
838366	0.5072623	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)
122147	0.5067128	
120749	0.5060444	ESTs, Moderately similar to KIAA1215 protein [H.sapiens]
855563	0.5059683	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
487733	0.5057167	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)
625693	0.5055986	hypothetical protein MGC10911

813751	0.5051993	sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)
842825	0.5047729	G1 to S phase transition 1
323693	0.5047237	adaptor-related protein complex 1, sigma 1 subunit
202514	0.5045411	DNA (cytosine-5-)-methyltransferase 3 alpha
1517749	0.5045134	ESTs
124331	0.5025464	cleavage and polyadenylation specific factor 5, 25 kD subunit
1474424	0.5021308	Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328
1848977	0.5015371	glycerol kinase
454896	0.5013449	DnaJ (Hsp40) homolog, subfamily A, member 2
1702742	0.5011725	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
746163	0.5009715	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
810734	0.4998276	polymerase (DNA-directed), delta 4
725284	0.4992842	phosphorylase kinase, gamma 2 (testis)
52103	0.4988158	hypothetical protein FLJ23045
739109	0.4986821	adaptor-related protein complex 2, sigma 1 subunit
488505	0.4981852	accessory proteins BAP31/BAP29
365060	0.4976091	RAB11A, member RAS oncogene family
41569	0.4974126	hypothetical protein FLJ12650
81336	0.4955353	uteroglobin
700792	0.4949149	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
1592715	0.4944665	Homer, neuronal immediate early gene, 3
142586	0.4942961	MCT-1 protein
261472	0.4941066	putative nuclear protein ORF1-FL49
246800	0.4927231	hypothetical protein FLJ10803
124298	0.4922937	microsomal glutathione S-transferase 3
1898619	0.4916939	hypothetical protein MGC15737
739126	0.4905859	tissue specific transplantation antigen P35B
376875	0.490328	flavin containing monooxygenase 1
358162	0.4901786	protein predicted by clone 23627
590759	0.4895021	sterol-C4-methyl oxidase-like

1947647	0.4887766	CGI-147 protein
120271	0.4886584	hypothetical protein MGC4692
488642	0.4881613	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
1492468	0.4878466	DEME-6 protein
345538	0.4875796	cathepsin L
344091	0.4871044	ESTs
123441	0.4862068	ribosomal protein L7a
202901	0.48608	vav 2 oncogene
757489	0.4859039	tubulin, alpha 2
49117	0.4856399	KIAA0215 gene product
812994	0.4854155	retinoid X receptor, alpha
731023	0.4853217	WD repeat domain 5
814899	0.4840969	BCL2/adenovirus E1B 19kD-interacting protein 3-like
756666	0.4835569	protein phosphatase 1, catalytic subunit, alpha isoform
2018337	0.4833207	glucosidase, beta; acid (includes glucosylceramidase)
1568825	0.4829928	Arg/Abl-interacting protein ArgBP2
869375	0.4827093	isocitrate dehydrogenase 2 (NADP+), mitochondrial
595213	0.4824381	hypothetical protein
744374	0.4824256	putative ankyrin-repeat containing protein
73009	0.4822587	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
70606	0.481356	ESTs
358456	0.4812268	Sec61 gamma
810762	0.4806851	SNARE protein
823930	0.4800704	actin related protein 2/3 complex, subunit 1A (41 kD)
2020898	0.4797032	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
564981	0.4782207	ESTs
1637282	0.4777562	hexokinase 2
855749	0.476968	triosephosphate isomerase 1
744944	0.4769116	myosin VI
263727	0.4767486	DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis
470092	0.476018	like-glycosyltransferase
782513	0.4759571	interferon, alpha-inducible protein (clone IFI-6-16)

897813	0.4749348	polyadenylate binding protein-interacting protein 1
141852	0.4748862	purinergic receptor P2Y, G-protein coupled, 2
855800	0.4748367	prolyl endopeptidase
41356	0.4746307	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
753320	0.4744893	hypothetical protein FLJ20533
784140	0.474314	WD repeat domain 15
530310	0.4739401	KIAA0143 protein
813387	0.4727653	diaphorase (NADH/NADPH) (cytochrome b-5 reductase)
358267	0.4719017	EST, Moderately similar to AF119917 63 PRO2831 [H.sapiens]
2018527	0.4717524	dolichyl-phosphate mannosyltransferase polypeptide 3
781342	0.4716127	hypothetical protein MGC11115
785707	0.4708376	protein regulator of cytokinesis 1
140635	0.4706227	ESTs
814306	0.4705205	tumor protein D52
784150	0.4702303	RAB31, member RAS oncogene family
839746	0.4699443	Homo sapiens, Similar to RIKEN cDNA 5830420C20 gene, clone IMAGE:3633379, mRNA, partial cds
377384	0.4698441	nuclear receptor subfamily 2, group F, member 2
183200	0.4697062	fumarylacetoacetate hydrolase (fumarylacetoacetase)
345423	0.4694596	DKFZP564M112 protein
204686	0.4687565	FXYD domain-containing ion transport regulator 1 (phospholemman)
428582	0.4684705	hypothetical protein FLJ20296
210862	0.4683996	acyl-Coenzyme A oxidase 1, palmitoyl
51741	0.4678807	GTP-binding protein
296702	0.4670993	deiodinase, iodothyronine, type I
840865	0.4666048	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)
278531	0.4663008	cytochrome c oxidase subunit VIc
60565	0.4659865	lethal giant larvae (Drosophila) homolog 2
1639531	0.4658349	RAB27A, member RAS oncogene family
346942	0.4657601	phosphatidylinositol glycan, class Q
884498	0.4648731	uncharacterized hypothalamus protein HT012

345787	0.4647372	highly expressed in cancer, rich in leucine heptad repeats
825296	0.4646099	low density lipoprotein receptor defect C complementing
2248488	0.4645687	ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate)
824962	0.4638758	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
843054	0.4637278	KIAA1533 protein
140289	0.4624364	hypothetical protein
1558233	0.4622449	ESTs
265592	0.4615543	activated RNA polymerase II transcription cofactor 4
767761	0.4608709	DKFZP434B168 protein
770766	0.4603527	DKFZP564C1940 protein
814209	0.4602081	ESTs
773674	0.4601667	oncogene TC21
703707	0.4599434	aspartate beta-hydroxylase
951216	0.4594172	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)
139354	0.4582974	hypothetical protein
79710	0.4579008	KIAA0174 gene product
823574	0.457224	endosulfine alpha
845363	0.4570873	non-metastatic cells 1, protein (NM23A) expressed in
283751	0.4567022	cortistatin
810156	0.4561539	deoxythymidylate kinase (thymidylate kinase)
1416782	0.4558415	creatine kinase, brain
810609	0.4551167	hypothetical protein PP1226
770675	0.454729	Homo sapiens cDNA: FLJ21323 fis, clone COL02374
626318	0.4529715	ubinuclein 1
38356	0.4513099	cytochrome P450, subfamily 46 (cholesterol 24-hydroxylase)
705064	0.4497555	transforming, acidic coiled-coil containing protein 3
127646	0.4493747	
299815	0.4482635	hypothetical protein DC42
815026	0.4472842	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD

489823	0.4468978	COX17 (yeast) homolog, cytochrome c oxidase assembly protein
469151	0.4462659	eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)
41826	0.4456463	ESTs
47853	0.445149	aldehyde dehydrogenase 4 family, member A1
144740	0.4449229	similar to phosphatidylcholine transfer protein 2
726658	0.4446657	non-metastatic cells 3, protein expressed in
325515	0.444486	hypothetical protein FLJ10980
815781	0.4441245	heat shock 105kD
746190	0.4430243	hypothetical protein DKFZp761B1514
2016194	0.4417536	glia maturation factor, beta
1584287	0.4413331	KIAA0241 protein
147834	0.4412795	zinc finger protein 217
154610	0.4410751	dynactin 4
754653	0.4405873	cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (Drosophila) homolog
742581	0.440367	Homo sapiens cDNA FLJ10366 fis, clone NT2RM2001420
2306987	0.4402912	secreted and transmembrane 1
878406	0.4396935	metaxin 1
430614	0.438809	2,3-bisphosphoglycerate mutase
415102	0.4387892	cell division cycle 25C
358217	0.4385343	glypican 4
1636669	0.4384707	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
83358	0.4380365	ESTs
1325816	0.4379227	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)
824524	0.4375695	UDP-galactose transporter related
795805	0.4370764	KIAA0332 protein
743977	0.4368155	Homo sapiens mRNA for TL132
785793	0.4367093	capping protein (actin filament) muscle Z-line, alpha 1
266218	0.4362517	hypothetical protein FLJ11350
769600	0.4362014	uracil-DNA glycosylase 2
1656062	0.4355127	coagulation factor XII (Hageman factor)
2017415	0.43546	centromere protein A (17kD)
772220	0.4352917	for protein disulfide isomerase-related

811907	0.4340842	hypothetical protein FLJ22056
789376	0.4339171	thioredoxin reductase 1
782503	0.4334388	fatty acid desaturase 1
753897	0.4324066	autocrine motility factor receptor
767289	0.4323485	hypothetical protein FLJ10055
1159963	0.4323117	interferon regulatory factor 7
1652310	0.4321289	Homo sapiens, clone MGC:19613 IMAGE:3833049, mRNA, complete cds
358936	0.4314082	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]
41698	0.4310061	progesterone binding protein
1635665	0.430087	Homo sapiens, RIKEN cDNA 2010100O12 gene, clone MGC:14813 IMAGE:4133274, mRNA, complete cds
1558642	0.4298376	hypothetical protein MGC2771
1733262	0.4289711	BLu protein
823694	0.4280476	Homo sapiens chromosome 19, BAC CIT-HSPC_204F22 (BC228680), complete sequence; contains bacterial insertion element
1641894	0.4277815	EST
2572170	0.4277651	ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans [C.elegans]
731080	0.4276128	hypothetical protein FLJ12661
649084	0.4275738	carbonic anhydrase XI
795498	0.4270889	putative transmembrane protein
897770	0.4270685	
2250839	0.4266248	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
510794	0.4264564	c-myc binding protein
825822	0.4255725	hypothetical protein
825659	0.424655	N-myc downstream regulated
826077	0.4242762	pyruvate dehydrogenase (lipoamide) beta
293727	0.4242722	hypothetical protein MGC861
503866	0.4230404	sperm autoantigenic protein 17
491527	0.4219324	Homo sapiens, Similar to CG7083 gene product, clone MGC:10534 IMAGE:3957147, mRNA, complete cds
292936	0.4217115	hypothetical protein FLJ10468

823940	0.4214277	transducer of ERBB2, 1
414992	0.420994	K562 cell-derived leucine-zipper-like protein 1
346134	0.4209894	calcium-regulated heat-stable protein (24kD)
51657	0.4208387	hypothetical protein ET
2009779	0.420743	rabaptin-5
1523225	0.4195302	oncostatin M receptor
826194	0.4177687	synaptotagmin-like 2
85804	0.4171445	hypothetical protein FLJ21918
725223	0.4167519	KIAA0077 protein
79726	0.4162264	ESTs, Highly similar to T46395 hypothetical protein DKFZp434I1120.1 [H.sapiens]
1762111	0.4160469	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
509588	0.4157059	TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD
327506	0.4152106	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 327506
744047	0.4151137	polo (Drosophia)-like kinase
221499	0.4149929	KIAA0508 protein
745394	0.4147627	Homo sapiens cDNA: FLJ23249 fis, clone COL04196
149539	0.4138942	KIAA1700
823907	0.4135955	hypothetical protein FLJ10511
66317	0.4132405	H1 histone family, member 2
295986	0.413087	emopamil-binding protein (sterol isomerase)
565235	0.4124667	spermine synthase
825386	0.4121622	ATP synthase, H+ transporting, mitochondrial F1F0, subunit d
250313	0.4121296	ESTs
72050	0.4114235	chloride channel, nucleotide-sensitive, 1A
417801	0.4112944	mitochondrial ribosomal protein L27
841501	0.4111707	KIAA0102 gene product
813707	0.410787	regulator of G-protein signalling 16
745083	0.4107735	ubiquitin specific protease 18
244974	0.4105439	hypothetical protein FLJ22875
26883	0.4103824	protein kinase (cAMP-dependent, catalytic) inhibitor beta

280249   0.4096162   Kruppel-like factor 7 (ubiquitous)
74738   0.409593   Homo sapiens, clone IMAGE:3535294, mRNA, partial cds

1753497   0.409432   ovo (Drosophila) homolog-like 1
204299   0.4073087   replication protein A3 (14kD)
358609   0.4071867   NADH dehydrogenase (ubiquinone) flavoprotein 3 (10kD)

290101   0.4071477   ESTs
2306221   0.4068933   wingless-type MMTV integration site family, member 10B

726439   0.4067151   CGI-143 protein
431805   0.405447   granulin
111362   0.4045961
472103   0.4043572   soc-2 (suppressor of clear, C.elegans) homolog

788444   0.4042598   KIAA0033 protein
1632252   0.404193   complement component 1, q subcomponent, alpha polypeptide

150118   0.4039789   hypothetical protein DKFZp434F054
594226   0.403676   Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409

1499828   0.4030396   fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase,
                       Bombay phenotype included)

810939   0.40256   hypothetical protein FLJ22169
841621   0.4020253   ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]

200144   0.4019827   ring-box 1
486110   0.4017126   profilin 2
292213   0.4014458   guanine nucleotide binding protein (G protein), beta polypeptide
                       2
1631132   0.401216   peptide transporter 3
669379   0.4011648   Homo sapiens BAC clone RP11-505D17 from 7p22-p21

773685   0.4009493   phosphodiesterase 4D interacting protein (myomegalin)

810411   0.400096   hypothetical protein FLJ13222
1583198   0.39981   ESTs, Weakly similar to S65824 reverse transcriptase homolog
                       [H.sapiens]
84295   0.3989864   interleukin 1 receptor antagonist
757328   0.3985331   hypothetical protein FLJ22678
35626   0.39822   Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955

1587863	0.3980812	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
713862	0.3965573	ubiquitin-protein isopeptide ligase (E3)
343731	0.3962504	
43977	0.3961848	KIAA0182 protein
78869	0.3954821	cell membrane glycoprotein, 110000M(r) (surface antigen)
756595	0.395121	S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
701115	0.3936994	hypothetical protein PRO2013
81599	0.3932769	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)
1636844	0.3926235	ring finger protein 14
703739	0.392298	nuclear cap binding protein subunit 1, 80kD
279633	0.3907503	ESTs, Highly similar to I38759 zinc finger/leucine zipper protein [H.sapiens]
122091	0.3903482	casein kinase 2, alpha 1 polypeptide
786067	0.390151	cell division cycle 25B
1909574	0.3900357	mitochondrial ribosomal protein S11
263013	0.3894536	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
491001	0.3884144	glyoxalase I
455275	0.3869874	hypothetical protein FLJ23469
85450	0.3868399	acyl-Coenzyme A oxidase 2, branched chain
773286	0.3861543	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1
366156	0.3861394	Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838
49630	0.3858335	calcium channel, voltage-dependent, L type, alpha 1D subunit
121251	0.385792	hypothetical protein MGC5576
2322223	0.3853156	small nuclear ribonucleoprotein polypeptide A
276915	0.3851081	DNA (cytosine-5-)-methyltransferase 3 beta
1591264	0.3849595	transaldolase 1
1434948	0.3849593	HIV TAT specific factor 1
489657	0.3847527	tryptophan rich basic protein

810947	0.3833137	LIS1-interacting protein NUDE1, rat homolog
298417	0.3833014	trefoil factor 3 (intestinal)
154707	0.3831976	MpV17 transgene, murine homolog, glomerulosclerosis
79032	0.3816428	CGI-82 protein
1916575	0.3814206	BCL2-interacting killer (apoptosis-inducing)
1585492	0.3812472	ESTs
1455394	0.3811391	cytochrome c
769942	0.3810371	kinesin-like 4
429387	0.3810004	chimerin (chimaerin) 2
768377	0.3809674	activity-dependent neuroprotective protein
214996	0.380548	ESTs
1557637	0.3805285	ESTs
1517595	0.3804132	KIAA0175 gene product
841260	0.3801713	hypothetical protein
491524	0.3785047	mitochondrial ribosomal protein L13
30170	0.3782337	caspase 3, apoptosis-related cysteine protease
76196	0.3781541	hypothetical protein FLJ20062
2017721	0.3781067	ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]
134918	0.3779855	ESTs
347726	0.377767	homeo box D8
1469148	0.3776558	FGFR1 oncogene partner
1649374	0.3771383	homogentisate 1,2-dioxygenase (homogentisate oxidase)
241043	0.3770901	Human clone 137308 mRNA, partial cds
815835	0.3764754	hypothetical protein R33729_1
143426	0.3764075	ras homolog gene family, member B
1412245	0.3762847	carboxypeptidase A2 (pancreatic)
786265	0.3760397	KIAA0750 gene product
266500	0.3758559	ESTs
755301	0.3749416	protein kinase C, delta
294397	0.3744208	DKFZP586A0522 protein
155806	0.3741516	
41123	0.3739475	Homo sapiens, Similar to RIKEN cDNA 2210021G21 gene, clone MGC:14859 IMAGE:3621871, mRNA, complete cds
454339	0.3738929	thiopurine S-methyltransferase

810316	0.3732635	very long-chain acyl-CoA synthetase; lipidosin
812105	0.3731726	ALL1-fused gene from chromosome 1q
773426	0.3727398	KIAA0391 gene product
1572710	0.3725734	hypothetical protein FLJ21213
772898	0.372064	ribosomal protein S15a
283739	0.3714571	Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838
289505	0.3714361	ESTs, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]
897177	0.3712716	phosphoglycerate mutase 1 (brain)
782547	0.3708058	ESTs
647866	0.3706822	Homo sapiens cDNA FLJ13975 fis, clone Y79AA1001585
1679942	0.3706798	KIAA1053 protein
566443	0.3705134	Homo sapiens cDNA FLJ12793 fis, clone NT2RP2002033
302996	0.3698028	chloride intracellular channel 3
726699	0.3695061	ESTs, Weakly similar to AAB47496 NG5 [H.sapiens]
2094232	0.3693257	chromosome 1 open reading frame 12
2549634	0.3692338	activator of S phase kinase
177827	0.3691459	synaptotagmin VII
852829	0.3691079	karyopherin alpha 3 (importin alpha 4)
207794	0.3679245	nuclear factor (erythroid-derived 2), 45kD
823909	0.3675927	
743810	0.3667087	hypothetical protein MGC2577
810039	0.3662086	defender against cell death 1
53039	0.3659853	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1
809727	0.365892	unc-51 (C. elegans)-like kinase 1
26171	0.3656147	KIAA0856 protein
1570663	0.3656056	FK506-binding protein 4 (59kD)
179212	0.3649976	ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]
292996	0.36439	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
259950	0.364359	hypothetical protein FLJ14991
815794	0.3643266	nucleobindin 2
965223	0.3642603	thymidine kinase 1, soluble

592801	0.3638731	serine palmitoyltransferase, long chain base subunit 2
42831	0.3638165	N-terminal kinase-like
788641	0.3638059	adaptor-related protein complex 1, sigma 2 subunit
813845	0.3637519	RNA, U transporter 1
52076	0.3633002	neuroblastoma (nerve tissue) protein
154493	0.3629466	interferon-induced protein 75, 52kD
1519013	0.3628651	Homo sapiens, clone IMAGE:3537447, mRNA, partial cds
1434905	0.3624537	homeo box B7
825282	0.3624112	DKFZP586L0724 protein
322617	0.3623149	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)
814353	0.3622592	phorbol-12-myristate-13-acetate-induced protein 1
2017917	0.360911	Homo sapiens cDNA: FLJ23371 fis, clone HEP16068, highly similar to HSTFIISH Homo sapiens mRNA for transcription elongation factor TFIIS
813616	0.3608471	FK506-binding protein like
1846982	0.3602851	inhibin, beta C
505289	0.3595549	angiotensin II, type I receptor-associated protein
1565079	0.358728	B-cell linker
795401	0.3573481	diacylglycerol O-acyltransferase (mouse) homolog
781047	0.357207	budding uninhibited by benzimidazoles 1 (yeast homolog)
346696	0.3570344	TEA domain family member 4
809466	0.3568464	DNA segment on chromosome 19 (unique) 1177 expressed sequence
743220	0.3566593	hypothetical protein FLJ12517
131268	0.3564734	growth factor receptor-bound protein 14
119133	0.3564449	Homo sapiens mRNA; cDNA DKFZp434B231 (from clone DKFZp434B231)
242706	0.3562469	Homo sapiens, Similar to RIKEN cDNA 5730494N06 gene, clone MGC:13349 IMAGE:4249231, mRNA, complete cds
66599	0.3561699	N-acetyltransferase 1 (arylamine N-acetyltransferase)
46716	0.3557556	ESTs

271899	0.355689	Ser-Thr protein kinase related to the myotonic dystrophy protein kinase
25440	0.3554359	staufen (Drosophila, RNA-binding protein) homolog 2
1899312	0.3551595	ESTs
783681	0.354881	upstream regulatory element binding protein 1
131091	0.3548154	Not56 (D. melanogaster)-like protein
300099	0.3547857	ESTs
588436	0.3544892	butyrate-induced transcript 1
2069602	0.3539588	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)
810959	0.3534647	Rho GDP dissociation inhibitor (GDI) alpha
649977	0.3534567	Homo sapiens clone CDABP0014 mRNA sequence
345069	0.3532976	nuclear factor (erythroid-derived 2)-like 3
767487	0.3530592	ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1
824943	0.3527414	hypothetical protein
744994	0.3526118	hypothetical protein FLJ12242
773381	0.3525581	N-ethylmaleimide-sensitive factor attachment protein, alpha
1568561	0.3518952	BCL2-like 1
2028916	0.3516982	Homo sapiens mRNA for Hmob33 protein, 3' untranslated region
753457	0.3515361	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)
2161427	0.3509243	progesterone receptor
1947381	0.3509235	hypothetical protein FLJ22329
82421	0.3506778	zinc finger protein 6 (CMPX1)
504461	0.3506753	opsin 3 (encephalopsin)
754625	0.3503938	ATPase, Class II, type 9A
795543	0.3500184	thioredoxin peroxidase (antioxidant enzyme)
1910316	0.3498986	KIAA0535 gene product
172785	0.3493683	NAG-5 protein
1910078	0.3491481	ESTs, Weakly similar to YK54_YEAST HYPOTHETICAL 18.4 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [S.cerevisiae]
321354	0.3489273	mitochondrial ribosomal protein L15

878815	0.3478601	ADP-ribosylation factor 3
741769	0.3475255	polymerase (DNA directed), beta
487831	0.3464379	Homo sapiens cDNA FLJ14059 fis, clone HEMBB1000573
754046	0.3464097	DNA segment on chromosome X (unique) 9879 expressed sequence
344988	0.3464047	
530093	0.3463461	myelin protein zero-like 1
823615	0.3462131	Homo sapiens cDNA: FLJ21245 fis, clone COL01184
144881	0.3461767	calumenin
128695	0.3455381	ESTs, Weakly similar to I38344 titin, cardiac muscle [H.sapiens]
884511	0.3440809	cytochrome c oxidase subunit VIIb
128711	0.3437491	anillin (Drosophila Scraps homolog), actin binding protein
470035	0.3436575	prokineticin 1 precursor
1568126	0.3434836	solute carrier family 37 (glycerol-3-phosphate transporter), member 1
588911	0.3427563	2',5'-oligoadenylate synthetase 1 (40-46 kD)
35191	0.3427094	stromal cell-derived factor 2
814989	0.3426862	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
73638	0.3425644	protein tyrosine phosphatase type IVA, member 2
1605178	0.3416196	amino acid transporter system A1
214068	0.3414185	GATA-binding protein 3
755599	0.3413351	interferon induced transmembrane protein 1 (9-27)
782439	0.3413092	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e
595070	0.3408109	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4
183440	0.3406314	arylsulfatase A
774502	0.3402891	protein tyrosine phosphatase, non-receptor type 12
235986	0.338857	wingless-type MMTV integration site family, member 11
289936	0.3382708	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
824108	0.3381616	SCAN domain-containing 1

26617	0.3371923	activated leucocyte cell adhesion molecule
810497	0.3367408	ESTs, Weakly similar to A35363 synapsin I splice form a [H.sapiens]
40042	0.3362557	hypothetical protein FLJ10747
811142	0.3361932	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
2046679	0.3358043	ESTs
487444	0.3357395	cyclic AMP phosphoprotein, 19 kD
78736	0.3354693	Homo sapiens clone 24877 mRNA sequence
1637302	0.3353374	DNAJ domain-containing
825606	0.335057	kinesin-like 1
76362	0.3349202	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
1883028	0.3345488	Homo sapiens mRNA; cDNA DKFZp434J1912 (from clone DKFZp434J1912)
789383	0.3341667	cAMP responsive element modulator
302549	0.3340582	basic transcription element binding protein 1
309288	0.334016	replication factor C (activator 1) 4 (37kD)
712314	0.3338146	myosin regulatory light chain interacting protein
241677	0.3332521	Homo sapiens, clone MGC:18110 IMAGE:4152745, mRNA, complete cds
898253	0.3331924	reticulocalbin 2, EF-hand calcium binding domain
770992	0.3331315	
81203	0.3328573	paraoxonase 3
416436	0.3325571	mitochondrial ribosomal protein L24
1660666	0.332029	carbonic anhydrase VB, mitochondrial
811582	0.3319191	golgi phosphoprotein 2
2054122	0.3318413	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3
837864	0.3314764	progestin induced protein
1632247	0.3312131	hypothetical protein FLJ23436
298143	0.3307258	ESTs
2027952	0.3307056	hypothetical protein FLJ20297
1600281	0.3304323	nucleolar protein 3 (apoptosis repressor with CARD domain)
814270	0.3300091	polymyositis/scleroderma autoantigen 1 (75kD)

415589	0.3296266	Homo sapiens clone PP1498 unknown mRNA
1912951	0.329484	uterine-derived 14 kDa protein
726637	0.3292392	t-complex-associated-testis-expressed 1-like
1474684	0.3291536	ephrin-A1
1843843	0.3290269	KIAA1304 protein
266312	0.3289707	ATPase, Cu++ transporting, beta polypeptide (Wilson disease)
135640	0.3288537	syntaxin 3A
279720	0.3282308	ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]
724888	0.3272422	cytochrome P450, subfamily IVB, polypeptide 1
811808	0.326728	nucleoside diphosphate kinase type 6 (inhibitor of p53-induced apoptosis-alpha)
131566	0.3261265	hypothetical protein MGC11061
154466	0.3258377	STIP1 homology and U-Box containing protein 1
1692195	0.3254467	smg GDS-ASSOCIATED PROTEIN
785368	0.3254362	PDZ-binding kinase; T-cell originated protein kinase
1637516	0.325364	nuclear autoantigen
1637829	0.3246232	ESTs
810567	0.3243984	Homo sapiens, clone MGC:3182 IMAGE:3356293, mRNA, complete cds
1027283	0.3242547	ESTs
306806	0.324179	Homo sapiens, Similar to hypothetical protein FLJ12838, clone IMAGE:4130879, mRNA, partial cds
855406	0.3241172	Homo sapiens clone TCCCIA00176 mRNA sequence
429222	0.3239231	CGI-107 protein
1500542	0.3228485	regulator of G-protein signalling 11
269606	0.3228482	N-methylpurine-DNA glycosylase
74566	0.3226444	exportin 1 (CRM1, yeast, homolog)
754192	0.3225824	Homo sapiens mRNA; cDNA DKFZp586H0924 (from clone DKFZp586H0924)
180785	0.322529	KIAA0726 gene product
824479	0.3225263	exonuclease NEF-sp
842863	0.3225116	N-myc downstream regulated
1708055	0.3225042	glioblastoma overexpressed